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MEDLINE=80145719; PubMed=6987665;
Volanakis J.E., Bhown A.S., Bennett J.C., Mole J.E.;
"Partial amino acid sequence of human factor D:homology with serine
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Johnson D.M.A., Gagnon J., Reid K.B.M.;
"Factor D of the alternative pathway of human complement.
Purification, alignment and N-terminal amino acid sequences
major cyanogen bromide fragments, and localization of the se
residue at the active site.";
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MEDLINE=94118317; PubMed=8289289;
Narayana S.V.L., Carson M., El-Kabbani O., Kilpatrick J.M. Chen X., Bugg C.E., Volanakis J.E., Delucas L.J.;
"Structure of human factor D. A complement system protein resolution.";
J. Mol. Biol. 235:695-708(1994).
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Johnson D.M.A., Gagnon J., Reid K.B.M.;
"Amino acid sequence of human factor D of the complement Similarity in sequence between factor D and proteases of origin.";
FEBS Lett. 166:347-351(1984).
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MEDLINE=81054886; PubMed=6776531;
Davis A.E. III;
"Active site amino acid sequence of human factor Proc. Natl. Acad. Sci. U.S.A. 77:4938-4942(1980).
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15-DEC-1998 (Rel. 37, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Complement factor D precursor (EC 3.4.21.46)
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MEDLINE=92250520; PubMed=1374388;
White R.T., Damm D., Hancock N., Rosen B.S.
Flier J.S., Spiegelman B.M.;
"Human adipsin is identical to complement at high levels in adipose tissue.";
J. Biol. Chem. 267:9210-9213(1992).
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Patent number W09006365, 14-JUN-1990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (2.0 ANGSTROMS)
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MEDLINE=85000441; PubMed=6383466;
Niemann M.A., Bhown A.S., Bennett J
"Amino acid sequence of human D of to
                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pathway.";
Biochemistry 23:2482-2486(1984)
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Proc. Natl. Acad. Sci. U.S.A.
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                                                  STANDARD;
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gamma).
Desmodus rotundus (Vampire bat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Chiroptera, Microchiroptera, Phyllostomidae,
Desmodontinae, Desmodus.
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KCRLYDVL (IN REF.
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    Q -> G (IN REF. 4).

TCNRRTHHDGAITE -> KCI
S -> T (IN REF. 3).
S -> H (IN REF. 3).
MISSING (IN REF. 4).
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Pred. No. 6.8e-06
); Mismatches 0
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01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Salivary plasminogen activator gamma precursor
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X MEDLINE=96025834; PubMed=7592653;
Kim S., Narayana S.V., Volanakis J.E.;
Kim S., Narayana S.V., Volanakis J.E.;

"Crystal structure of a complement factor D mutant expressing
T "Crystal structure of a complement factor D mutant expressing
T enhanced catalytic activity.";
J. Biol. Chem. 270:24399-24405(1995).

J. Biol. Chem. 270:24399-24405 (1995).

-!- FUNCTION: Factor D cleaves factor B when the latter is complexed
with factor C3b, activating the C3bbb complex, which then becomes
the C3 convertase of the alternate pathway. Its function is
homologous to that of C1s in the classical pathway.

-!- CATALYITC ACTIVITY: Cleaves component factor B (Arg-|-Lys) when in
complex with C3b or with cobra venom factor (CVF).

-!- SIMILARITY: Belongs to peptidase family S1.

-!- CAUTION: In addition to the conflicts shown in the feature table,
Ref.3 sequence had a peptide in the wrong order and another one
missing.
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PIR; A40197; DBHU.
PDB; 1DFP; 25-FEB-98.
PDB; 1DST; 11-JUL-96.
PDB; 1DSU; 17-AUG-96.
PDB; 1DIC; 22-JUN-99.
PDB; 1FDP; 03-DEC-99.
PDB; 1HFD; 22-JUN-99.
MEROPS; S01.191; -.
Genew; HGNC:2771; DF.
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vampire bat): unique fibrin specificity.";
Ann. N.Y. Acad. Sci. 667:395-403(1992).
-!- FUNCTION: Probably essential to support the feeding hat
exclusively haematophagous animal. Probable potent thro
                                                                  CHARACTERIZATION.
WEDLINE=93393059; PubMed=1309059;
Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petr:
Kraetzschmar J., Haendler B., Langer G., Baldus B., Witt W
                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Elthe European Bioinformatics Institute. There are no restiuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-sortsend an email to license@isb-sib.ch).
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SUBUNIT: Monomer.
SIMILARITY: Belongs to peptidase family SISIMILARITY: Contains 1 kringle domain.
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                 TISSUE=Salivary gland;
MEDLINE=92039036; PubMed=1937019;
Kraetzschmar J., Haendler B., Langer G. Alagon A., Donner P., Schleuning W.D.;
"The plasminogen activator family from vampire bat Desmodus rotundus: cloning Gene 105:229-237(1991).
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NCBI_TaxID=9430;
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CATALYTIC ACTIVITY: Specific cleavage of Arg- -Val bond plasminogen to form plasmin.

SUBUNIT: Monomer.

SIMILARITY: Belongs to peptidase family S1.

SIMILARITY: Contains 1 EGF-like domain.

SIMILARITY: Contains 1 kringle domain.
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"Plasminogen activators from the saliva of Desmodus rotu vampire bat): unique fibrin specificity.";
Ann. N.Y. Acad. Sci. 667:395-403(1992).
-!- FUNCTION: Probably essential to support the feeding exclusively haematophagous animal. Probable potent t
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01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Salivary plasminogen activator beta precursor
                                                                         Score 13; DB
Pred. No. 1e-
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TISSUE=Salivary gland;
MEDLINE=92039036; PubMed=1937019;
Kraetzschmar J., Haendler B., Langer G.,
Alagon A., Donner P., Schleuning W.D.;
"The plasminogen activator family from th
vampire bat Desmodus rotundus: cloning an
Gene 105:229-237(1991).
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Schleuning W.-D., Alagon A., Boidol F
Kraetzschmar J., Haendler B., Langer
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MEROPS; S01.239; -.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Pfam; PF00008; EGF; 1.

Pfam; PF00051; kringle; 1.

Pfam; PF00089; trypsin; 1.

PRINTS; PR00122; CHYMOTRYPSIN.

PRINTS; PR00181; EGF; 1.

SMART; SM00130; KR; 1.

SMART; SM00020; Tryp SPc; 1.

SMART; SM00020; Tryp SPc; 1.

PROSITE; PS00022; EGF_1; 1.

PROSITE; PS00021; KRINGLE 1; 1.

PROSITE; PS00021; KRINGLE 2; 1.

PROSITE; PS00134; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN HIS; 1.

PROSITE; PS00135; TRYPSIN SER; 1.
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SERINE PROTEASE.
CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
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Pred. No. 1.1e-05;
); Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O9ER04; Q9ER02; Q9ER03;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Transmembrane protease, serine 5 (EC 3.4.21.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).

TISSUE=Brain;

Mitsui S., Yamaguchi N.;

"cDNA cloning of mouse spinesin.";

Submitted (JUL-1998) to the EMBL/GenBank/DDBJ
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SEQUENCE FROM N.A. (ISOFORM
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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(POTENTIAL).
(POTENTIAL).
TISSUE=Brain;
Mitsui S., Yamaguchi N.;
"Molecular cloning of mouse type 4 spinesin.";
"Molecular cloning of mouse type 4 spinesin.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Type II membrane protein (Potential)
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=4;
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MEMBRANE
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SRCR.
SERINE PROTEASE
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CHARGE RELAY SYSTEM (ICHARGE (POTENTIAL).

BY SIMILARITY.

BY SIMILARITY.
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N-LINKED (GLCNAC...
Missing (in isoform 2
/Frid=VSP 005395.
Missing (in isoform 3
/Frid=VSP 005396.
Missing (in isoform 3
/Frid=VSP 005396.
Missing (in isoform 1
/Frid=VSP 005397.
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CYTOPLASMIC (PO
SIGNAL-ANCHOR (PO (POTENTIAL).
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                                                                                                                                                                                                                         Sequence=VSP_005397,
                                                                                                                                                                                                                                                                    Sequence=VSP_005395;
                                                                                                                                                          Name=4;
IsoId=Q9ER04-1; Sequence=Displayed;
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MGD; MGI:1933407; Tmprss5.

InterPro; IPR009003; Cys Ser_trypsin.

InterPro; IPR001254; Peptidase_S1.

InterPro; IPR001314; Peptidase_S1A.

InterPro; IPR001190; Srcr_receptor.

Pfam; PP00089; trypsin; 1.

PRINTS; PR00722; CHYMOTRYPSIN.

SMART; SM00020; Tryp_SPC; 1.

PROSITE; PS00134; TRYPSIN DOM; 1.

PROSITE; PS00135; TRYPSIN SER; 1.

PROSITE; PS00420; SRCR_1; FALSE_NEG.

PROSITE; PS00420; SRCR_1; FALSE_NEG.

PROSITE; PS00420; SRCR_2; 1.

Hydrolase; Serine protease; Transmembrar Glycoprotein; Alternative splicing.

DOMAIN.
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EMBL; AB016230; BAB20277.1; -.
EMBL; AB016423; BAB20278.1; -.
EMBL; AB041037; BAB40328.1; -.
HSSP; P00763; 1DPO.
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                                                                                                                                                                                                                     Chordata; Craniata; Vertebrata; Butele Primates; Catarrhini; Hominidae; Homo
3LVEEAWKP -> MEAQVGLLWV (in
FTId=VSP 005398.
-> G (IN REF. 1; BAB20277)
5CFC31789C6899AA CRC64;
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                                                                                                                                                                                           (Spinesin)
                                                                                                                                                                                                                                                                                    Okui A., Yamada T., Nakazato H., Mitsui S., 1855, a novel transmembrane serine protease,
                                                               Indels
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                                            Length
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Predominantly
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OR (TYPE-II
                                                                                                                                                                                                                                                                                                              iol. Chem. 277:6806-6812(2002).
SUBCELLULAR LOCATION: Type II membrane protein (TISSUE SPECIFICITY: Brain-specific. Predominantl neurons, in their axons, and at the synapses of
                                                     05;
                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Transmembrane protease, serine 5 (EC 3.4.21.-)
                                                                                                                                                                                                                                                                                                                                                   spinal cord.
SIMILARITY: Belongs to peptidase family S1
SIMILARITY: Contains 1 SRCR domain.
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                                                               Mismatches
                                              Score 13;
Pred. No.
         /FTId=VSP
D -> G (IN
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PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPc; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
PROSITE; PS00420; SRCR 1; FALSE NEG.
PROSITE; PS50287; SRCR 2; FALSE NEG.
Hydrolase; Serine protease; Transmemba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEROPS, S01.313; -.
InterPro; IPR009003; Cys Ser_trypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR001190; Srcr_receptor.
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HSSP; P00763; 1DPO.
Genew; HGNC:14908; TMPRSS5.
MIM; 606751; --
MEROPS; S01.313; -.
                          49632 MW;
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                                                               Conservative
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                                                                                          Yamaguchi N., Okui A "Spinesin/TMPRSS5, a human spinal cord.";
                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                              (Human)
                            AA;
                                                      Similarity
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PubMed=11741986;
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16-OCT-2001
16-OCT-2001
28-FEB-2003
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TISSUE=Salivary gland;
MEDLINE=92039036; PubMed=1937019;
Kraetzschmar J., Haendler B., Langer G., Boidol W., Bringmann P., Alagon A., Donner P., Schleuning W.D.;
"The plasminogen activator family from the salivary gland of the vampire bat Desmodus rotundus: cloning and expression.";
Gene 105:229-237(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                activation cleavage.";
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TISSUE=Salivary gland;
MEDLINE=98022741; PubMed=9354616;
Renatus M., Stubbs M.T., Huber R., Bringmann P., Donner P.,
Schleuning W.D., Bode W.;
"Catalytic domain structure of vampire bat plasminogen activator:
molecular paradigm for proteolysis without activation cleavage.";
molecular paradigm for proteolysis without activation cleavage.";
Biochemistry 36:13483-13493(1997).

-I- FUNCTION: Probably essential to support the feeding habits of
exclusively haematophagous animal. Potent thrombolytic agent.
-I- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
plasminogen to form plasmin.
                           SIMILARITY).
SIMILARITY).
SIMILARITY).
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Desmodus rotundus (Vampire bat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Chiroptera; Microchiroptera; Phyllostomidae;
Desmodontinae; Desmodus.
NCBI_TaxID=9430;
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(POTENTIAL).
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Baldus B., Witt W
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GE (POTENTIAL).
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1.2e-05;
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                                                     CHARGE RELAY SYSTE
CLEAVAGE (POTENTINE)
BY SIMILARITY.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
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vampire bat): unique fibrin specificity.
Ann. N.Y. Acad. Sci. 667:395-403(1992).
                                                                                                                                                                                                                                                                                    13;
No
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CHARGE
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MEDLINE=93393059; PubMed=1309059;
Schleuning W.-D., Alagon A., Boidol
Kraetzschmar J., Haendler B., Langer
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Similarity
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Best Local S
Matches 13
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(EC 3.4.21.68) (DSPA
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P15638;
01-APR-1990 (Rel. 14, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
alpha-2) (BAT-PA) (T-plasminogen activator).
Desmodus rotundus (Vampire bat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Phyllostomidae;
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1.2e-05;
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/FTId=CAR_000028.
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SMART; SM00020; Tryp SPc; 1.

PROSITE; PS0126; EGF 2; 1.

PROSITE; PS0026; EGF 3; 1.

PROSITE; PS0021; KRINGLE 1; 1.

PROSITE; PS00021; KRINGLE 1; 1.

PROSITE; PS00021; KRINGLE 2; 1.

PROSITE; PS00134; TRYPSIN DOM; 1.

PROSITE; PS00135; TRYPSIN HIS; 1.

PROSITE; PS00135; TRYPSIN SER; 1.

PROSITE; PS00136; TRYPSIN SER; 1.
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ENZYME REGULATION: Activity toward plasminogen is stimul the presence of fibrin I.
SUBUNIT: Monomer.
DOMAIN: The fibronectin type-I domain mediates binding tand the kringle domain apparently mediates fibrin-induce stimulation of activity.
SIMILARITY: Belongs to peptidase family S1.
SIMILARITY: Contains 1 EGF-like domain.
SIMILARITY: Contains 1 fibronectin type I domain.
SIMILARITY: Contains 1 kringle domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SALIVARY PLASMINOGEN ACTIVATOR FIBRONECTIN TYPE-I. EGF-LIKE.
                                                                                                             This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMI the European Bioinformatics Institute. There are no restriuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
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GlycoSuiteDB; P98119; -.
InterPro; IPR009003; Cye Ser trypsin.
InterPro; IPR006209; EGF_like.
InterPro; IPR006210; IEGF.
InterPro; IPR006210; Kringle.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1.
Pfam; PF00008; EGF; 1.
Pfam; PF00089; fn1; 1.
Pfam; PF00089; trypsin; 1.
ProDom; PD000395; Kringle; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR0018; KRINGLE.
ProDom; PD000395; Kringle; 1.
SMART; SM00180; KR; 1.
SMART; SM00130; KR; 1.
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EMBL; M63986; AAA31592.1; -
PIR; JS0597; JS0597.
PDB; 1A51; 23-MAR-99.
MEROPS; S01.232; -.
GlycoSuiteDB; P98119; -.
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SEQUENCE FROM N.A.
MEDLINE=88087303; PubMed=2826484;
Rickles R.J., Darrow A.L., Strickland S.;
"Molecular cloning of complementary DNA to mouse tissue plasminogen
                                                                                                                                                                                                                                                                                                                                        SALIVARY PLASMINOGEN ACTIVATOR ALPHA 2. FIBRONECTIN TYPE-I.
EGF-LIKE.
KRINGLE.
SERINE PROTEASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
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Signal; Multigene family.
POTENTIAL.
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Mismatches 0;
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SMART; SM00181; EGF; 1.

SMART; SM00058; FN1; 1.

SMART; SM00020; Tryp SPc; 1.

PROSITE; PS00022; EGF 1; 1.

PROSITE; PS00026; EGF 2; 1.

PROSITE; PS00026; EGF 3; 1.

PROSITE; PS00021; KRINGLE 1; 1.

PROSITE; PS00021; KRINGLE 1; 1.

PROSITE; PS00134; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN HIS; 1.

PROSITE; PS00134; TRYPSIN HIS; 1.

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vampire bat): unique fibrin specificity.";
Ann. N.Y. Acad. Sci. 667:395-403(1992).
-!- FUNCTION: Probably essential to support the feeding habits
exclusively haematophagous animal. Probable potent thrombol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          agent.

CATALYTIC ACTIVITY: Specific cleavage of Arg- -Val bond in plasminogen to form plasmin.

ENZYME REGULATION: Activity toward plasminogen is stimulate the presence of fibrin I.

SUBUNIT: Monomer.
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TISSUE=Salivary gland;

MEDLINE=90036867; PubMed=2509450;

Gardell S.J., Duong L.T., Diehl R.E., York J.D., Hare T.R., Register R.B., Jacobs J.W., Dixon R.A.F., Friedman P.A.;

"Isolation, characterization, and cDNA cloning of a vampire salivary plasminogen activator.";

J. Biol. Chem. 264:17947-17952(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN: The fibronectin type-I domain mediates binding and the kringle domain apparently mediates fibrin-inducstimulation of activity.

SIMILARITY: Belongs to peptidase family S1.

SIMILARITY: Contains 1 EGF-like domain.

SIMILARITY: Contains 1 fibronectin type I domain.

SIMILARITY: Contains 1 kringle domain.
                                                                                                                                              Bringma
                                                                                                                                                                                  salivary gland
expression.";
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Schleuning W.-D., Alagon A., Boidol W., Bringmann P.,
Kraetzschmar J., Haendler B., Langer G., Baldus B., V
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PIR; A34369; A34369.
PIR; JS0598; JS0598.
HSSP; P98119; 1A51.
MEROPS; S01.232; -.
InterPro; IPR009003; Cy8_Ser_trypsin.
InterPro; IPR000083; Fibrnctn1.
InterPro; IPR000083; Fibrnctn1.
InterPro; IPR000001; Kringle.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
                                                                                                                    MEDLINE=92039036; PubMed=1937019; Kraetzschmar J., Haendler B., Langer G. Alagon A., Donner P., Schleuning W.D.; "The plasminogen activator family from vampire bat Desmodus rotundus: cloning Gene 105:229-237(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00722; CHYMOTRYPSIN
PRINTS; PR00018; KRINGLE.
ProDom; PD000395; Kringle; 1.
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                           Desmodus
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                                                                                                     TISSUE=Salivary gland;
MEDLINE=92039036; Pubm
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CHARACTERIZATION
                           esmodontinae; D
CBI TaxID=9430;
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**REDILINE=22388257; PubMed=12477932;

**REDILINE=22388257; PubMed=12477932;

**REDILINE=22388257; PubMed=12477932;

**REDILINE=22388257; PubMed=12477932;

**REDILINE=22388257; PubMed=12477932;

**RIAUSDER R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

**A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

**RIAUSDER R.D., Colling F.S., Wagner L., Schaefer C.F., Batchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

**Rapleton M.J., Ordan H., Moore T., Mar. Rubin G.M., Hong L.,

**Rapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

**Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

**Robarder S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

**A Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,

**A Villalon D.K., Muzny D.M., Sodergren E.J., Lu K., Gibbs R.A.,

**A Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

**A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

**Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

**A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

**Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-!- FUNCTION: Converts the abundant, but inactive, zymogen plasminogen to plasmin by hydrolyzing a single Arg-Val bond in plasminogen. By controlling plasmin-mediated proteolysis, it plays an important role in tissue remodeling and degradation, in cell migration and many other physiopathological events.

-!- CATALYTIC ACTIVITY: Specific cleavage of Arg-{-Val bond in plasminogen to form plasmin.
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PTM: THE SINGLE CHAIN, ALMOST FULLY ACTIVE ENZYME, CAN BE FURT PROCESSED INTO A TWO-CHAIN FULLY ACTIVE FORM BY A CLEAVAGE AFT ARG-308 CATALYZED BY PLASMIN, TISSUE KALLIKREIN OR FACTOR XA.

MISCELLANEOUS: Binds to the kringle structure of the fibrin A chain. Binding to fibrin enhances its catalytic activity.
cell
 expression during F9 teratocarcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: Heterodimer of chain A and chain B held by a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Belongs to peptidase family S1.
SIMILARITY: Contains 1 EGF-like domain.
SIMILARITY: Contains 1 fibronectin type I domain.
SIMILARITY: Contains 2 kringle domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR009003; Cys Ser trypsin
InterPro; IPR006209; EGF_like.
InterPro; IPR000083; Fibrnctn1.
                   differentiation.";
J. Biol. Chem. 263:1563-1569(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000001; Kringle.
InterPro; IPR001254; Peptidase !
InterPro; IPR001314; Peptidase .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; fn1; 1.
1; kringle; 2.
9; trypsin; 1.
722; CHYMOTRYPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; J03520; AAA40470.1; -
EMBL; BC011256; AAH11256.1;
PIR; A29941; A29941.
HSSP; P00750; 1A5H.
MEROPS; S01.232; -.
 and its
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MGI:97610; Plat.
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PF00051; kr
PF00089; tr
S; PR00722;
                                                                                                  FROM N.A
  activator mRNA
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CHAIN.
FIBRONECTIN TYPE-I.
EGF-LIKE.
KRINGLE 1.
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PLASMINOGEN
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P19637;
01-FEB-1991 (Rel. 17, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tissue-type plasminogen activator precursor (EC (t-PA) (t-plasminogen activator).
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N-LINKED (GLCNAC.
G -> A (IN REF. 1
P -> A (IN REF. 1
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Pred. No. 1.4e-
0; Mismatches
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BY SIMILARITY.
               SMART; SM00181; EGF; 1.

SMART; SM00181; EGF; 1.

SMART; SM00020; Tryp SPc; 1.

PROSITE; PS00022; EGF 1; 1.

PROSITE; PS00022; EGF 2; 1.

PROSITE; PS00026; EGF 3; 1.

PROSITE; PS00021; KRINGLE 1; 2.

PROSITE; PS00021; KRINGLE 1; 2.

PROSITE; PS00021; KRINGLE 1; 2.

PROSITE; PS00034; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN HIS; 1.

PROSITE; PS00135; TRYPSIN HIS; 1.

PROSITE; PS00135; TRYPSIN SER; 1.
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TISSUE-TYPE
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       ProDom;
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Glycoprotein;
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PLASMINOGEN ACTIVATOR
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Pfam; PF00008; EGF; 1.

Pfam; PF00039; fn1; 1.

Pfam; PF00081; kringle; 2.

Pfam; PF00089; trypsin; 1.

PRINTS; PR00018; KRINGLE.

ProDom; PD000395; Kringle; 2.

SMART; SM00130; KR; 2.

SMART; SM00130; KR; 2.

SMART; SM00020; Tryp SPC; 1.

SMART; SM00020; Tryp SPC; 1.

PROSITE; PS00126; EGF 3; 1.

PROSITE; PS01253; FIBRONECTIN 1; 1.

PROSITE; PS00126; EGF 3; 1.

PROSITE; PS00126; EGF 3; 1.

PROSITE; PS00134; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN DOM; 1.

PROSITE; PS00135; TRYPSIN ER; 1.

PROSITE; PS00136; EGF 3; 1.

ROSITE; PS00136; TRYPSIN ER; 1.

PROSITE; PS00136; TRYPSIN ER; 1.
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KRINGLE 2.
SERINE PROTEASE.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
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P00750; Q15103;
21-JUL-1986 (Re
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TPA HUMAN
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nd for commercial
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EMBL outstation
                                                                                                                                                                                                                                                                                                                                                          Feng P., Ohlsson M., Ny T.;

"The structure of the TATA-less rat tissue-type plasminogen activator gene. Species-specific sequence divergences in the promoter predict differences in regulation of gene expression.";

J. Biol. Chem. 265:2022-2027(1990).

-!- FUNCTION: Converts the abundant, but inactive, zymogen plasminogen to plasmin by hydrolyzing a single Arg-Val bond in plasminogen. By controlling plasmin-mediated proteolysis, it plays an important role in tissue remodeling and degradation, in cell migration and many other physiopathological events.

-!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in plasminogen to form plasmin.

-!- SUBUNIT: Heterodimer of chain A and chain B held by a disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAN BE FURTHER
CLEAVAGE AFTER
R FACTOR XA.
the fibrin A
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                                                                               , Rattus
                                                            stomi;
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1- PTM: THE SINGLE CHAIN, ALMOST FULLY ACTIVE ENZYME, CAN BE PROCESSED INTO A TWO-CHAIN FULLY ACTIVE FORM BY A CLEAVAGY ARG-308 CATALYZED BY PLASMIN, TISSUE KALLIKREIN OR FACTOR :- MISCELLANEOUS: Binds to the kringle structure of the fibrichain. Binding to fibrin enhances its catalytic activity.
1- SIMILARITY: Belongs to peptidase family S1.
1- SIMILARITY: Contains 1 EGF-like domain.
1- SIMILARITY: Contains 2 kringle domains.
                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=89170114; PubMed=3148445;
Ny T., Leonardsson G., Hsueh A.J.W.;
"Cloning and characterization of a cDNA for rat tissue-type plasminogen activator.";
Dlasminogen activator.";
                                                            Craniata; Vertebrata; Euteleo
Sciurognathi; Muridae; Murina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Elthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
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Kringle.
Peptidase_S
Peptidase_S
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EGF_like.
Fibrnctn1.
                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
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EMBL; M31197; AAA42261.1; -
EMBL; M31185; AAA42261.1; JG
EMBL; M31186; AAA42261.1; JG
EMBL; M31189; AAA42261.1; JG
EMBL; M31189; AAA42261.1; JG
EMBL; M31190; AAA42261.1; JG
EMBL; M31191; AAA42261.1; JG
EMBL; M31192; AAA42261.1; JG
EMBL; M31194; AAA42261.1; JG
EMBL; M31195; AAA42261.1; JG
EMBL; M31196; AAA4
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Pro; IPR009003; CPro; IPR006209; Pro; IPR006210; IPR006210; IPR0; IPR006210; Pro; IPR001254; Pro; IPR001354; Pro; IPR001354; Pro; IPR001314;
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Nucleic Acids Res. 18:1086-1086(1990).
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                                                                                                                       SEQUENCE TISSUE=Melanoma;
TISSUE=Melanoma;
MEDLINE=83115262; PubMed=6337343;
MEDLINE=83115262; PubMed=6337343;
Pennica D., Holmes W.E., Kohr W.J., Harkins R.N., Vehar G.A., Pennica D., Holmes W.E., Yelverton E., Seeburg P.H., Heyneke Ward C.A., Bennett W.F., Yelverton E., Seeburg P.H., Heyneke Mard C.A., Bennett W.F., Yelverton E., Seeburg P.H., Heyneke
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"Cloning and expression of human tissue-type plasminogen act cDNA in E. coli.";
Nature 301:214-221(1983).
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MEDLINE=84298137; PubMed=6089198;
Ny T., Elgh F., Lund B.;
"The structure of the human tissue-type plasminogen activate correlation of intron and exon structures to functional and
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DNA 6:461-472(1987).
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Harris T.J., Patel T., Marston F.A., Little S., Emtage J.S., Opdenakker G., Volckaert G., Rombauts W., Billiau A., Somer "Cloning of cDNA coding for human tissue-type plasminogen and its expression in Escherichia coli.";
Mol. Biol. Med. 3:279-292(1986).
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Н
                                                                      Euteleo
21-JUL-1986 (Rel. 01, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Tissue-type plasminogen activator precursor (EC 3.4.21.68)
(t-PA) (t-plasminogen activator) (Alteplase) (Reteplase).
                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=86196143; PubMed=3009482;
Friezner Degen S.J., Rajput B., Reich E.;
"The human tissue plasminogen activator gene.";
J. Biol. Chem. 261:6972-6985(1986).
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MEDLINE=90192129; PubMed=2107528;
Siebert P.D., Fong K.;
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Reddy V.B., Garramone A.J., Sasa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 domains.";
. Acad. Sci. U.S.A.
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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

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"Generation and initial analysis of more than 15,000 full-length

proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Pohl G., Kaellstroem M., Bergsdorf N., Wallen P., Joernvall H.;
Pohl G., Kaellstroem M., Bergsdorf N., Wallen P., Joernvall H.;
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derived amino acid sequence, identify the active site serine residue,
establish glycosylation sites, and localize variant differences.";
Biochemistry 23:3701-3707(1984).
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MEDLINE=91291340; PubMed=1368681;
Itagaki Y., Yasuda H., Morinaga T., Mitsuda S., Higashio K.;
"Purification and characterization of tissue plasminogen activator secreted by human embryonic lung diploid fibroblasts, IMR-90 cells.' Agric. Biol. Chem. 55:1225-1232(1991).
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Harris R.J., Leonard C.K., Guzzetta A.W., Spellman M.W.;
"Tissue plasminogen activator has an O-linked fucose attached
threonine-61 in the epidermal growth factor domain.";
Biochemistry 30:2311-2314(1991).
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MEDLINE=90092112; PubMed=2513186;
Pfeiffer G., Schmidt M., Strube K.-H., Geyer R.;
"Carbohydrate structure of recombinant human uterine tissue plasminogen activator expressed in mouse epithelial cells.";
Eur. J. Biochem. 186:273-286(1989).
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MEDLINE=85289338; PubMed=3161893;
Fisher R., Waller E.K., Grossi G., Thompson D.,
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U.S.A. 80:349-352(1983)
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MEDLINE=83169656; PubMed=6572897;
Edlund T., Ny T., Raanby M., Heden L.-O.,
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MEDLINE=83209620; PubMed=6682760;
Wallen P., Pohl G., Bergsdorf N., R
"Purification and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Biochem. 132:681-686(1983)
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MEDLINE=91244765; PubMed=1645336,
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Proc. Natl. Acad. Sci.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Byeon I.-J.L., Kelley R.F., Llinas M.;
"IH NMR structural characterization of a recombinant kringle
from human tissue-type plasminogen activator.";
Biochemistry 28:9350-9360(1989).
                                                                                                                                                                                                                                                                                                                                                                         STRUCTURE D. MEDLINE=91200042; PubMed=1901/00,
MEDLINE=91200042; PubMed=1901/00,
Byeon I.-J.L., Kelley R.F., Llinas M.;
"Kringle-2 domain of the tissue-type plasminogen activator.
"Kringle-2 domain of the tissue-type plasminogen activator.
assignments and secondary structure.";
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"Disulfide pairing of the recombinant kringle-2 domain of plasminogen activator produced in Escherichia coli."; J. Biol. Chem. 266:10070-10072(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                  X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF CATALYTIC DON
MEDLINE=97449126; PubMed=9305622;
Renatus M., Engh R.A., Stubbs M.T., Huber R., Fischer
                                                                                                                                                                            proenzyme activity
                                                                         요;
                                                                                                                                                                                                                            MEDLINE=92118803; PubMed=1310033; de Vos A., Ultsch M.H., Kelley R.F., Padmanabhan K., Westbrook M.L., Kossiakof A.A.; "Crystal structure of the kringle 2 domain of tissue activator at 2.4-A resolution."; Biochemistry 31:270-279(1992).
                                                                                             domain
                                                                                           "The 2.3 A crystal structure of the catalytic domain two-chain human tissue-type plasminogen activator."; J. Mol. Biol. 258:117-135(1996).
                                                      CATALYTIC
                                                                                                                                                                                                                    N
                                                                         S., Rudolph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             red. No. 1.4e-05;
Mismatches 0;
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                                                                                                                                                                                                                     (2.4 ANGSTROMS) OF KRINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
1.4e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Tissue-type plasminogen activator precursor (t-PA) (t-PA) (t-PA).
                                                                                                                                                                           "Lysine 156 promotes the anomalous proenzyme crystal structure of single-chain human tPA. EMBO J. 16:4797-4805(1997).
                                                      QF)
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No.
                                                                        Lamba D., Bauer M., Huber R., Fischer
                                                      APHY (2.3 ANGSTROMS)
PubMed=8613982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92106329; PubMed=1762144; Byeon I.-J.L., Llinas M.; "Solution structure of the tissue 2 domain completed."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        222:1035-1051(1991)
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                                                      X-RAY CRYSTALLOGRAPHY
MEDLINE=96200985; Pub
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Best Local Similarity
Matches 13; Conser
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Q28198;
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01-NOV-1997
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                                                                              Bode W.;
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J. Mol.
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
Bovidae; Bovinae; Bos.
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JOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94242782; PubMed=8186251; Shibuya Y., Semba U., Okabe H., Kambara T., Yamamoto T.; Shibuya Y., Semba U., Okabe H., Kambara T., Yamamoto T.; "Primary structure of bovine Hageman factor (blood coagulat XII): comparison with human and guinea pig molecules."; Biochim. Biophys. Acta 1206:63-70(1994).
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PLASMINOGEN ACTIVAT
              PLASMINOGEN ACTIVAT
                                                                                                                                                                                                               (POTENT (POTENT)
                                                                                                                                                                                                                                            Length 566;
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01-FEB-1996 (Rel. 33, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Coagulation factor XII precursor (EC 3.4.21.38) (Hageman (HAF) (Fragment).
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                                                                                                                                                                    SIMILARITY)
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N-LINKED (GLCNAC. . .) (PO
2EB6BEB4E32276C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a serum glycoprotein that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 10-21; 350-364 AND 525-550.
MEDLINE=77182112; PubMed=861210;
Fujikawa K., Walsh A.K., Davie W.E.;
"Isolation and characterization of bovine factor XII
                                                                      SYSTEM.
SYSTEM.
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Mismatches 0;
                                                                CHARGE RELAY SYSTEM
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SSUE-TYPE
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                             FIBRONECTIN
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Pred. No
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SERINE F
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Biochemistry 16:2270-2278(1977)
-! - FUNCTION: Factor XII is a s
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34
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Best Local
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Matches
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a collaboration
            generation of bradykinin and angiotensin.

-!- CATALYTIC ACTIVITY: Cleaves selectively Arg-|-ile bonds in factor VII to form factor XI to form factor XI a.

-!- PTM: O- AND N-GLYCOSYLATED (BY SIMILARITY).
-!- MISCELLANBOUS: Factor XII, prekallikrein, and HMW kininogen form a complex bound to an anionic surface. Prekallikrein is cleaved by factor XII to form kallikrein, which then cleaves factor XII first to alpha-factor XIIa and then to beta-factor XIIa. Alpha-factor XIIa activates factor XII to factor XIIa as it lacks the trypsin/kallikrein cleavage site.
-!- SIMILARITY: Belongs to peptidase family S1.
-!- SIMILARITY: Contains 1 fibronectin type II domain.
-!- SIMILARITY: Contains 1 fibronectin type II domain.
-!- SIMILARITY: Contains 1 kringle domain.
                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Zymogen; Signal.
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ALPHA-FACTOR XIIA HEAVY C
ALPHA-FACTOR XIIA LIGHT C
FIBRONECTIN TYPE-II.
EGF-LIKE 1.
FIBRONECTIN TYPE-I.
EGF-LIKE 2.
fibrinolysis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REBLI, SYJOL64; AABJORGALL;

RESP; PO0763; 1DPO.

RECOPS; S01.211;

LICETPC; IPRO06209; EGF_like.

INTERPC; IPRO06210; IEGF.

INTERPC; IPRO01254; Peptidase_S1.

INTERPC; IPRO01254; Peptidase_S1.

INTERPC; IPRO01314; Peptidase_S1A.

PÉAM; PPO0049; EGF; 2.

REPCO; PRO0049; EAL; 1.

REPCO; PRO0049; EAR; 2.

REPCO; PRO0059; FNI; 1.

REPCO; PROO175; PROMOCC; EGF_1; 2.

REPCO; PROO175; PROMOCC; EGF_1; 2.

REPCO; PROO175; PROMOCC; EGF_1; 3.

REPCO; PROS175; PSO0021; RERCOMECTIN 1; 1.

REPCO; PROS175; PSO0013; FIRENOMECTIN 2; 1.

REPCO; PROS175; PSO00134; TRYPSIN ERR; 1.

REPCO; PROS175; PSO00134; TRYPSIN ERR; 1.

REPCO; PROS175; PSO00134; TRYPSIN ERR; 1.

REPCOSTF; PSO00134; TRYPSIN ERR; 1.

REPCOSTF; PRO0135; TRYPSIN ERR; 1.

REPCOSTF; PRO0135; TRYPSIN ERR; 1.

REPCOSTF; PRO0135; TRYPSIN ERR; 2.

REPCOSTF; PRO0135; TRYPSIN ERR; 2.

REPCOSTF; PRO0134; TRYPSIN ERR; 2.

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REPCOSTF; PRO0135; TRYPSIN ERR; 2.
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S45281.
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593
78
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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1; Signal.
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Zymogen;
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FIBRONECTIN TYPE-II.
FIBRONECTIN TYPE-I.
FIBRONECTIN TYPE-I.
FIBRONECTIN TYPE-I.
FIBRONECTIN TYPE-I.
CHARGLE.
FRO-RICH.
SERINE PROTEASE.
CHARGE RELAY SYSTEM (BY SCHARGE RELAY 
                 I domain.
II domain.
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               fibronectin type
fibronectin type
kringle domain.
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  EGF-like domains
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m; Plasma; Kr
''''re domain;
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PIR, S28941; S28941.
HSSP; P00763; 1DPO.
MEROPS; S01.211; -..
InterPro; IPR001903; Cys Ser_trypsin.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001803; Fibrncth.
InterPro; IPR001804; Fibrncth.
InterPro; IPR001805; FN Type_II.
InterPro; IPR0018154; Peptidase_S1.
InterPro; IPR001814; Peptidase_S1.
InterPro; IPR001814; Peptidase_S1.
InterPro; IPR001814; Peptidase_S1.
InterPro; IPR001814; Peptidase_S1A.
Pfam; PF00008; EGF; 2.
Pfam; PF00008; EGF; 2.
Pfam; PF00008; EGF; 1.
PROMITS; PR0013; FNIYEII.
PRINTS; PR0013; FNIYEII.
PRINTS; PR0013; FNIYEII.
PRODOM; PD0000995; FNI; 1.
PRODOM; PD0000995; FNI; 1.
PROSITE; PS00022; EGF; 2.
PROSITE; PS00022; EGF; 2; 1.
PROSITE; PS00022; EGF 3; 2.
PROSITE; PS00023; FIBRONECTIN_2; 1.
PROSITE; PS00023; FIBRONECTIN_2; 1.
PROSITE; PS00023; FIBRONECTIN_2; 1.
PROSITE; PS00021; KRINGIE_1; 1.
PROSITE; PS00023; FIBRONECTIN_1; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROMAIN 359 603 ALPHA-FACT
DOMAIN 359 603 ALPHA-PACT
DOMAIN 310 320 603 PALPA-PACT
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  Sembara...

A Sembara T., Vamamoto T., Kunisada T., Shibuya Y., Tanase S.,

Kambara T., Okabe H.;

Kambara T., Okabe H.;

Teleavage site differs from the human molecule.";

Biochim. Biophys. Acta 1159:113-121(1992).

L. FUNCTION: Factor XII is a serum glycoprotein that participates in the initiation of blood coagulation, fibrinolysis, and the generation of bradykinin and angiotensin.

C.-!- FUNCTION: Factor XII is a serum glycoprotein that participates in the initiation of blood coagulation, fibrinolysis, and the generation of bradykinin and angiotensin.

C.-!- CATALYTIC ACTIVITY: Cleaves selectively Arg-|-Ile bonds in factor VII to form factor XII, prekallikrein, and HWW kininogen form a complex bound to an anionic surface! Prekallikrein is cleaved by factor XII to form kallikrein, which then cleaves factor XII first to alpha-factor XII and then to beta-factor XIIa. Alpha-factor XII activates factor XI to factor XIa.

C.-!- SIMILARITY: Belongs to peptidase family SI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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Hystricognathi; Caviidae;
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(BY
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COLINKED (FUC) (BY S)
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SYSTEM
SYSTEM
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, Last sequence update)
, Last annotation update)
   KRINGLE.
PRO-RICH.
SERINE PROTEASE.
CHARGE RELAY SYS'
CHARGE RELAY SYS'
                                                              CHARGE RELAY S
CHARGE RELAY S
BY SIMILARITY.
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MEDLINE=93003367; PubMed=1390917;
Semba U., Yamamoto T., Kunisada T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
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Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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ilarity 100.0%;
Conservative
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B-1996 (Rel. 33, La
R-2004 (Rel. 43, La
lation factor XII p
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Catarrhini; Hominidae; Homo.
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Cool D.E., McGillivray R.T.A.;
"Characterization of the human blood coagulation factor XII
Intron/exon gene organization and analysis of the 5'-flankin
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Nucleic Acids Res. 14:3146-3146(1986).
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Mismatches 0;
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Cool D.E., Edgell C.-J.S., Louie G.V.,
McGillivray R.T.A.;
"Characterization of human blood coagu."
Prediction of the primary structure of
structure of beta-factor XIIa.";
J. Biol. Chem. 260:13666-13676(1985).
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MEDLINE=86176794; PubMed=3754331;
Tripodi M., Citarella F., Guida S
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the initiation of blood coagulation, fibrinolysis, and the the initiation of blood coagulation, fibrinolysis, and the the initiation of blood coagulation, fibrinolysis, and the generation of bradykinin and angiotensin.

-!- CATALYTIC ACTIVITY: Cleaves selectively Arg-|-11e bonds in factor VII to form factor VIIa and factor XI to form factor XIa.

-!- PTM: O- AND N-GLYCOSYLATED.
-!- DISEASE: Defects in F12 do not cause any clinical symptoms. The sole effect is that whole-blood clotting time is prolonged.
-!- MISCELLANEOUS: Factor XII, prekallikrein, and HMW kininogen form a complex bound to an anionic surface. Prekallikrein is cleaved by factor XII to form kallikrein, which then cleaves factor XII first to alpha-factor XII and then to beta-factor XIIa. Alpha-factor XII activates factor XI to factor XIa.

-!- SIMILARITY: Contains 2 EGF-like domains.
-!- SIMILARITY: Contains 1 fibronectin type I domain.
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WARIANT TENRI CYS-53.

MEDLINE=99290785; PubMed=10361128;

Kondo S., Tokunaga F., Kawano S., Oono Y., Kumagai S., Koide T.;

Kondo S., Tokunaga F., Kawano S., Oono Y., Kumagai S., Koide T.;

"Factor XII Tenri, a novel cross-reacting material negative factor XII

deficiency, occurs through a proteasome-mediated degradation.";

Blood 93:4300-4308(1999).

-I- FUNCTION: Factor XII is a serum glycoprotein that participates in the initiation of blood coagulation, fibrinolysis, and the
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the factor
material
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                                                                                                                                                                                                                                                                                                                                                                       Lutze G., Lammle a 11396 (G-->A) in in cross-reacting
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MEDLINE=94325559; PubMed=8049433;
Hovinga J.K., Schaller J., Stricker H., Wuillemin W.A.,
Laemmle B.;
                  for human factor XII
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Harris R.J., Ling V.T., Spellman M.W.;
"O-linked fucose is present in the first domain of factor XII but not protein C.";
J. Biol. Chem. 267:5102-5107(1992).
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MEDLINE=83291041; PubMed=6604055;
Fujikawa K., McMullen B.A.;
"Amino acid sequence of human beta-fi
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                a cDNA coding
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                                                                                                                                                          (activated Hageman factor).";
J. Biol. Chem. 260:5328-5341(1985)
                                                                                    SEQUENCE OF 20-379.
MEDLINE=85182674; PubMed=3886654;
McMullen B.A., Fujikawa K.;
"Amino acid sequence of the heavy
                                                                                                                                                                                                                                                                                                                                      TISSUE=Blood;
MEDLINE=96133302; PubMed=8528215;
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MEDLINE=90046788; PubMed=2510163;
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E.W.;
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                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EGF-LIKE 2.
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EMBL; M17466; AAB59490.1; -.
EMBL; M17464; AAB59490.1; -.
EMBL; M17465; AAB59490.1; JOINED.
EMBL; M13147; AAA70224.1; -.
EMBL; U71274; AAB51203.1; -.
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MEROPS; S01.211; -.
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Q7t0x2 xenopus lae Q8cj16 rattus norv Q9pvx7 xenopus lae Q9bzwl homo sapien Q8cj17 rattus norv	3dr 199 7k8	sus scroors	O35727 mus musculu Q80yc5 mus musculu	Sug 1	4 mus muscul	4 xenopus	poltenia v	scirpoph	drosophil	drosophila	rhyzoperth	stomoxys		hypoderma	rhyzopert	drosophil	drog	drosoph
Q7T0X2 Q8CJ16 Q9PVX7 Q9BZW1 Q8CJ17	QBCDRO Q9BU99 O86YK8	Q8SQ23 Q8MKB1	035727 Q80YC5	Q81ZZ5 Q97507	Q8VCS4	091674	QBMVL.1	Q911K4 O45045	QBSXZ4	Q8MKZ1	Q9XYY0	076520	Q9Y7A9	Q25081	Q9XYY1	018599	Q9W5U8	бэлере
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Best Local
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                                                   RESULT
Q7ZT70
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D
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SEQUENCE FROM N.A.

STRAIN=CS7BL/60; TISSUE=Tongue;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,

Kawai J., Shinagawa A., Shibata K., Yonno H., Adachi J., Fukuda S.,

Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Koshiwa H.,

A Salto T., Okazaki Y., Gojobori T., Bano H., Kasukawa T., Saito R.,

A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Bozuki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Nordone P., Ring B., Ringwald M., Weitz C., Whittaker C., Wilming L.,

Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Havsehizaki V.
   LIDHRWVLTA
                ||||||||||
|:IDHRWVLTA
                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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of a full-length mouse cDNA collecti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IEA
                                                                                                                                                                                            update)
                                                                                                                                                                  (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 25, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 31; DB 11; I Pred. No. 1.1e-23; ); Mismatches 0;
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GO; GO:0004263; F:chymotrypsin activity; IEA.

GO; GO:0008233; F:peptidase activity; IEA.

GO; GO:0004295; F:trypsin activity; IEA.

GO; GO:0006508; P:proteolysis and peptidolysis;

InterPro; IPR009003; Cys_Ser_trypsin.

InterPro; IPR001254; Peptidase_S1.

InterPro; IPR001314; Peptidase_S1A.
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"Functional annotation of a full-length mous
Nature 409:685-690(2001).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY
EMBL; AK009217; BAB26143.1; -.
HSSP; P00763; 1DPO.
MEROPS; S01.020; -.
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PROSITE; PS50240; TRYPSIN DOM;
PROSITE; PS00134; TRYPSIN HIS;
PROSITE; PS00135; TRYPSIN SER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              trypsin; 1.
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                                                                                                                                             PRELIMINARY;
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Rest Locai Similarity
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                                                   AHCSG
                                                                            AHCSG
                                                                                                                                                                                                                                   Mus musculus
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09CV76,
01-JUN-2001
01-JUN-2001
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MEDLINE=2253355; PubMed=12707349;
A Endo Y., Nonaka M., Saiga H., Kakinuma Y., Mateusita A., Takahashi M., Amtausinine=2253355; PubMed=12707349;
Endo Y., Nonaka M., Saiga H., Kakinuma Y., Mateusita A., Takahashi M., Mateusinine M., Saiga H., Kakinuma Y., Mateusita M., Fujita T., Saiga H., Kakinuma Y., Mateusita M., Saiga H., Saiga H., Saiga M., Saiga H., Saiga M., Saiga M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lampetra japonica (Japanese lamprey) (Entosphenus japonicus).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Lethenteron.
NCBI_TaxID=94989;
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                                                                                                                                                                                                                                                                        01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mannose-binding lectin associated serine protease-1
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SMART; SM00179; EGF_CA; 1.

SMART; SM00020; Tryp_SPc; 1.

PROSITE; PS00070; ALDEHYDE DEHYDR CYS; 1.

PROSITE; PS01180; CUB; 2.

PROSITE; PS01187; EGF_CA; 1.

PROSITE; PS00134; TRYPSIN_HIS; 1.

PROSITE; PS00134; TRYPSIN_HIS; 1.

PROSITE; PS00135; TRYPSIN_HIS; 1.
PRT;
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01-JUN-2003
01-JUN-2003
01-OCT-2003
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235 AA;
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Matches 13; Conser
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Best Local S
Matches 13
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                                                                                                                                                                                                                                                            Mateui H., Takahashi T.;
Mateui H., Takahashi T.;
Mateui H., Takahashi T.;
Mateui H., Takahashi T.;
Mus musculus mRNA for serine protease-like gene spliced variant:
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
EMBL; AB047758; BAB63919.1; -.
HSSP; P00761; 1AN1.
MEROPS; S01.106; -.
MGD; MGI:1920586; 1700036D21Rik.
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase S1A.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                         Craniata; Vertebrata; Euteleost
Sciurognathi; Muridae; Murinae;
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SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Protease; Serine protease.
SEQUENCE 200 AA; 22135 MW; 972959E4686EF603 CRC64;
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L; BC034529; AAH34529.1; -.
GO:0004263; F:chymotrypein activity; IEA.
GO:0008233; F:peptidase activity; IEA.
GO:0004295; F:trypein activity; IEA.
GO:0006508; P:proteolysis and peptidolysis; IEA.
erPro; IPR009003; Cye Ser_trypsin.
erPro; IPR001254; Peptidase_S1.
erPro; IPR001314; Peptidase_S1A.
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Last annotation update)
                                                                                               Last sequence update)
Last annotation update)
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5.8e-05;
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Strausberg R.;
Strausberg (JUL-2002) to the EMBL/GenBank/DDBJ (Submitted (JUL-2002) to PEPTIDASE FAMILY S1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 11
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                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.2%;
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                                                                               19,
19,
25,
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                                                                              (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 DACQGDSGGPLVC
                                                                                                                                    Serine protease-like 1 1700036D21RIK.
                                                                                                                                                                          (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 13; Conser
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                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QBN4E0;
01-OCT-2002
01-OCT-2002
01-OCT-2003
                                                            Q924U6;
01-DEC-2001
01-DEC-2001
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
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InterPro;
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Q8N4E0;
01-OCT-
                                            Q924U6
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Q8N4E0
          RESULT
                           Q924U6
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
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0
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Pfam; PF00089; trypsin; 1.

PRINTS; PR00722; CHYMOTRYPSIN.

SMART; SM00020; Tryp_SPc; 1.

PROSITE; PS50240; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_HIS; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

Hypothetical protein; Hydrolase; Protease; Serine protease.

NON_TER 1
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Q86VJ5
Q86VJ5;
Q86VJ5;
Q1-JUN-2003 (TrEMBLrel. 24, Last sequence update)
Q1-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Q1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to D component of complement (Adipsin) (Fragment)
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutely
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                      9DEF67A48D5913F6 CRC64
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on update)
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Strausberg R.;
Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ datak
EMBL; BC044756; AAH44756.1; -.
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IE
InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
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Pred. No. 6.7e-05;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 11
                                                                                                                                                                                                                                                                                                                                                                                                                                 Q80VS4;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence up
01-OCT-2003 (TrEMBLrel. 25, Last annotation
Similar to kallikrein 14 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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No.
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Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tumor;
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Mammalia; Butheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26059 MW;
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                                                                                                                                                        25110 MW;
                                                                                                                                                                                              5.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FROM N.A.
IRI; TISSUE=Breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       208
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13; Conser
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Q9W7Q5;
01-NOV-1999
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Q9W7Q5
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MatBui H., TakahaBhi T.; "MatBui H., TakahaBhi T.; "MouBe serine protease preferentially expressed in brain."; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67F02995119490BC CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

TISSUE=Spleen;
Strausberg R.;
Strausberg R.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ datak
EMBL; BC051001; AAH51001.1; -.
GO; GO:0004263; F:chymotrypein activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEI
InterPro; IPR009003; Cys Ser_trypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
                                                                                                                                                                                                                                                                                                                                  sequences.";
id. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ore 13; DB 4; Lered. No. 6.9e-05; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    246 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM;
PROSITE; PS00134; TRYPSIN_HIS;
PROSITE; PS00135; TRYPSIN_HIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              trypain; 1.
2; CHYMOTRYPSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25809 MW;
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08,
25,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198 GDSGGPLVCGGVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protease (BSP)
OR MBSP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
13; Conser
                                                                                                                                                                                                                                                                                                                                                 Acad.
                  FROM N.A
                                                                                                                                                                                                                                                                                                                                   and mouse cDNA
Proc. Natl. Aca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF00089;
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TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1998
01-OCT-2003
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nact Local
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PRSS18
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Gaps
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Trypsinogen 3.
Paralichthys olivaceus (Flounder).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Actinopterygii; Percomorpha; Pleuronectiformes; Pleuronectoidei; Paralichthyidae; Paralichthys.
NCBI TaxID=8255;
                                                                                                                                                                                                                                                                               in brain."
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                                                                                                                                                                    SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
A Matsui H., Takahashi T.;
Matsui H., Takahashi T.;
Matsui H., Takahashi T.;
Matsui H., Takahashi T.;

"The sequences of mouse serine protease gene expressed in b
I submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
C -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
SR EMBL; AB015206; BAA28895.1; -.
DR EMBL; Y18723; CAA77269.1; -.
DR EMBL; AB012402; BAA84544.1; -.
DR MGD; MGI:1343166; Prss18.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0006293; F:peptidase activity; IEA.
DR GO; GO:0006295; F:trypsin activity; IEA.
DR GO; GO:0006295; F:trypsin activity; IEA.
DR GO; GO:0006299; F:trypsin activity; IEA.
DR InterPro; IPR001314; Peptidase_S1.
DR InterPro; IPR001224; Peptidase_S1.
DR InterPro; PR00122; CHYMOTRYPSIN.
THATA:
PR00122; CHYMOTRYPSIN.
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TISSUE=Pancreas;
Suzuki T., Srivastava A.S., Kurokawa T.;
"Japanese flounder mRNA for trypsinogen 3.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB029752; BAA82364.2; -.
HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indel
SEQUENCE FROM N.A.
STRAIN=BALB/C; TISSUE=Skin;
Meier N., Dear T.N., Boehm T.;
"A novel serine protease expressed in the hair follicle submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E20C080087139B63 CRC64;
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GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis;
InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR001254; Peptidase_S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 13; DB 11;
Pred. No. 7e-05;
); Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPc; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
Hydrolase; Protease; Serine protea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%;
Matches 13; Conservative
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InterPro; IPR001254; Per
InterPro; IPR001314; Per
Pfam; PF00089; trypsin;
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                                                    NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                          QBWZB4;
01-MAR-2002
01-MAR-2002
01-OCT-2003
                                                                                                                                                                                                                            InterPro;
Pfam; PF0(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae
NCBI_TaxID=10090;
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                                                                                           Length 247
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SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
SEQUENCE 250 AA; 27016 MW; F62FEBF2290FEBE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                          CRC64;
InterPro; IPkuollin; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPc; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
Aydrolase; Protease; Serine protease.
                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                       DB 13;
7e-05;
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                                                                                          Score 13; DB
Pred. No. 7e-
0; Mismatches
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                                                                                                                                                                                                                                                                                                                    Olsson A.Y., Lundwall A.; "Organization and evolution of the
                                                                                                                                                                                                                                                                                                            PubMed=12437987
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O54854;
01-JUN-1998 (TrEMBLrel. 06,
                                                                                             5.2%;
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                                                                                                                                          194 DACQGDSGGPLVC
                                                                                                                               DACQGDSGGPLVC
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Submitted (SEP-2002)
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nes 13; Conser
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                                                                                            Query Match
Best Local Similarity
Matches 13; Conser
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Pfam; PF00089;
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QBCGR5;
01-MAR-2003
01-MAR-2003
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Matches
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Gaps
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myelencephalon specific protease.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                    SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

X STRAINE=Sprague-Dawley;

MEDLINE=97477435; PubMed=9334391;

A Scarisbrick I.A., Towner M.D., Isackson P.J.;

A Scarisbrick I.A., Towner M.D., Isackson P.J.;

A Scarisbrick I.A., Towner M.D., Isackson P.J.;

T scarisbrick I.A., Towner M.D., Isackson P.J.;

I wervous system-specific expression of a novel serine protease:

T regulation in the adult rat spinal cord by excitotoxic injury.";

J. Neurosci. 17:8156-8168(1997).

C -! - SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.

R HSSP; P00763; 1DPO.

R HSSP; P00763; 1DPO.

R HSSP; P00763; 1DPO.

R HSSP; P00763; F:chymotrypsin activity; IEA.

GO; GO:0004263; F:trypsin activity; IEA.

GO; GO:0004295; F:trypsin activity; IEA.

GO; GO:0006509; P:proteolysis and peptidolysis; IEA.

InterPro; IPR001314; Peptidase_S1A.

R InterPro; IPR001314; Peptidase_S1A.
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injury.";
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Last annotation update)
precursor (EC 3.4.21.46)
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ datab
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
EMBL; AJ313463; CAC48304.1; -.
HSSP; P00761; 1AN1.
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0008233; F:complement factor D activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IE?
InterPro; IPR001254; Peptidase SI.
InterPro; IPR001314; Peptidase SIA.
InterPro; IPR001314; Peptidase SIA.
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Pred. No. 7.1e-05;
); Mismatches 0;
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Catarrhini;
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01-MAR-2002 (TrEMBLrel. 20, Last seque
01-0CT-2003 (TrEMBLrel. 25, Last annot
Adipsin/complement factor D precursor
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SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Protease; Serine protease SEQUENCE 251 AA; 28014 MW; E219
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Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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llarity 100.0%;
Conservative (
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Homo sapiens (Human)
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Best Local Similarity
Matches 13; Conser
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PRT;
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Suzuki Y., Sugano S., Hashimoto
"Isolation of full-length cDNA c
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                                                                                                                                                                                                                                                                                                                                                                                                                    CHYMOTRYPSIN.
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13; Conservative (
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                        PRELIMINARY;
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                                                                                                                                                                            SEQUENCE FROM N.A. TISSUE=Cerebellum;
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01-MAY-1999
01-MAY-1999
01-OCT-2003
                                     Q9MZZ6;
01-OCT-2000
01-OCT-2000
01-OCT-2003
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Best Local S
Matches 13
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Pfam; PF0
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RESULT
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae
NCBI_TaxID=10090;
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                                                                                                                              Length
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Strausberg R.;
Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databa
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

R EMBL; AB008928; BAB55605.1; -.

R HSSP; B00761; 1AN1.

R HSSP; B00761; 1AN1.

R MGD; MGI:1343166; Prass18.

GO; GO:0004263; F:Chymotrypsin activity; IEA.

GO; GO:0004295; F:trypsin activity; IEA.

GO; GO:0004295; F:trypsin activity; IEA.

GO; GO:0006508; P:proteolysis and peptidolysis; IEA

DR InterPro; IPR00903; Cys Ser trypsin.

DR InterPro; IPR001254; Peptidase S1.

InterPro; IPR00134; Peptidase S1.

DR PRINTS; PR00722; CHYMOTRYPSIN.

DR PROSITE; PS00134; TRYPSIN DOM; 1.

DR PROSITE; PS00135; TRYPSIN SER; 1.

KW Hydrolase; Protease; Serine protease.

SEOUENCE 253 AA; 28329 WW; CSEF98C7EEF2FBC1 CR
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Last annotation update)
18).
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7.1e-05;
                                                                                        ADIPSIN/COMPLEMENT 78B06C209DEEA362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protease, Neurosin.";
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ
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Pred. No. 7.10; Mismatches
                                                                                                                              Score 13; DB Pred. No. 7.1; Mismatches
             SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Protease; Serine protease; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE=Brain;
Mitsui S., Yamaguchi N.;
"cDNA cloning and characterization of
                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                Score
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   CHYMOTRYPSIN
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27033 MW;
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Best Local Similarity
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Best Local Similarity
                                                                                                        253 AA;
     PR00722;
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                                                                                                                                                                                                                                                                                                                                                            Mus musculus
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Q91Y82;
01-DEC-2001
01-DEC-2001
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RESULT Q91Y82

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                                                                                                                                                                       Hypothetical protein.
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
NCBI_TaxID=9541;
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SEQUENCE FROM N.A.
Sohn Y.-D., You W.K., Kim K.Y., Chung K.H., Park D.-H.;
Sohn Y.-D., You W.K., Kim K.Y., Chung K.H., Park D.-H.;
Cloning of a cDNA for a novel plasminogen activator from a K centipede Scolopendra.";
Centipede Scolopendra.";
L Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
C -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
R EMBL; U79521; AAD00320.1; -.
R HSSP; P00763; 1DPO.
R HSSP; P00763; 1DPO.
R GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
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Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
EMBL; AB046651; BAB03569.1; -.
HSSP; P00763; 1DPO.
MEROPS; S01.299; -.
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR001314; Peptidase_S1A.
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PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
Hypothetical protein; Hydrolase; Protease; Serine protestical protein; Hydrolase; Protestical protestical protein; Hydrolase; Protestical protestical protein; Hydrolase; Protestical protein; Hydrolase; Protein; Protein; Hydrolase; Protein; Hydrolase; Protein; Protein; Protein; Hydrolase; Protein; Protein; Hydrolase; Protein; Hydrolase; Protein; Protein; Protein; Hydrolase; Protein; P
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Plasminogen activator sPA.
Scolopendra subspinipes.
Scolopendra, Metazoa; Arthropoda; Myriapoda; Chilopoda;
Pleurostigmophora; Scolopendromorpha; Scolopendridae;
NCBI_TaxID=55038;
                                                                            (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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Pred. No. 7.5e-05;
); Mismatches 0;
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267 AA
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5.2%; Score 13; DB 5; Length 277;
Best Local Similarity 100.0%; Pred. No. 7.7e-05;
Matches 13; Conservative 0; Mismatches 0; Indels
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Protease; Serine protease.
SEQUENCE 277 AA; 30172 MW; EC62F80C8CBB246C CRC64;
                                                                                                                                                                                                                                                                                                                                                                194 DACQGDSGGPLVC 206
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212 DACQGDSGGPLVC 224
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Search completed: June 15, 2004, 16:25:17 Job time : 46 secs

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Compugen Ltd
version - 2004
GenCore
Copyright (c) 1993
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1135.976 Million cell June 15, 2004, 16:21:37 Run on:

US-10-006-856A-194

248

.. GVYTYICKYVDWIRMIMRNN

248 1 MGLSIFLLLCVLGLSQAATP. Perfect score: Title:

Sequence:

Gapext 60.0 Gapop 60.0 , OLIGO Scoring table:

96191526 residues 283366 Beqs, Searched:

0

Word size

283366 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Listing first

Database

pir 78:* 1: pir1:* 2: pir2:* 3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	<u>}</u>		omplement factor	plasminogen act	-plasminogen act	-plasminogen act	-plasminogen act	-plasminogen act	-plasm	-plasminogen act	-plasminogen act	oagulation facto	oagulation facto	bagulation fact	olyprotein - Afr	omplement facto	rypsin-like prot	rypsin-like prot	rypsin-like pro	Bin (EC 3.4.2	erine proteinase	rypsin (EC 3.	rypsin (EC 3.4.2	rypsin (EC 3.4.2	sin (EC 3.4.2	able serine	ymotrypsin-lik	able serin	erine proteinase	(EC 3.	neuropsin - mouse
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chymotrypsin-like trypsin-like prote	cell trypt	ryptase (EC 3.4.	ryptase (EC 3.4.	ryptase (EC 3.4.	ryptase (EC 3.4.	se (EC 3.4.	Be (EC 3.4	ell prote	on fact	sin (EC 3.	oagulation facto	asminogen act	nogen ac	asminogen act
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ALIGNMENTS

KENDLIL
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lement factor I
 N,Alternate names: adipsin; C3 convertase activator
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 985 #
197; A00
amm,
67, 9210
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 A; Accession: A40197
 A; Molecule type: mRNA
 A, Residues: 1-246 <whi></whi>
 GB: M845
The state of the s

A): Kiemmann, M.A.; Bhown, A.S.; Bennett, J.C.; Volanakis, J.E.

B. Nichmann, M.A.; Bhown, A.S.; Bennett, J.C.; Volanakis, J.E.

B. Diochemistry 23, 2482-2486, 1984

A): Title: Amino acid sequence of human D of the alternative complement pathway.

A): Recession. A00936; MUID:85000441; PMID:6383466

A): Recession. A00936; MUID:85000441; PMID:6383466

A): Recession. A00936

A): Recession. A00936; MUID:85000441; PMID:6383466

A): Recession. A00936

A): Title: Molecule type: protein

A): Recession. A004. O.; Inagi, R.; Sugiyama, S.; Miyama, A.; Maeda, K.; Nakashima, I.;

MOI. Immunol. 27, 637-644, 1990

A): Title: Molecule type: protein

A): Recession. A0071; MUID:90370044; PMID:2395435

A): Recession. A0071; MUID:90370044; PMID:2395435

A): Receive number: A0071; MUID:90370044; PMID:2395435

A): Residues: 19-20, XXX, 23-27, XXX, 30-31, XXX, 34, XX, 36-40 cMIY

A): Residues: 19-20, XXX, 23-27, XXX, 30-31, XXX, 34, XX, 36-40 cMIY

A): Residues: 19-20, XXX, 23-27, XXX, 30-31, XXX, 34, XX, 36-40 cMIY

A): Residues: 19-20, XXX, 23-27, XXX, 30-31, XXX, 34, XX, 36-40 cMIY

A): Residues: 19-20, XXX, 23-27, XXX, 30-31, XXX, 34, XX, 36-40 cMIY

A): Residues: 19-20, XXX, 23-27, XXX, 30-31, XXX, 34, XX, 36-40 cMIY

A): Residues: 19-20, XXX, 23-27, XXX, 30-31, XXX, 34, XX, 36-40 cMIY

A): Residues: 19-20, XXX, 23-27, XXX, 30-31, XX, 34, XX, 34,

Query Match

Length 246; 1; DB 13; Score 5.2%; ö

Gaps

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Indels

Length

plasi

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;87-120/Domain: EGF homology <EGF>
;128-209/Domain: kringle homology <FRG>
;128-209/Domain: kringle homology <FRY>
;226-471/Domain: trypsin homology <FRY>
;42-72,70-79,87-98,92-109,111-120,128-209,149-191,180-204,214-345,257-273,265-334,35
;153,398/Binding site: carbohydrate (Asn) (covalent) #status predicted
;225-226/Cleavage site: His-Ser (plasmin) #status predicted
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C; Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C; Accession: JSO597
R; Kraetzschmar, J; Haendler, B:; Langer, G; Boidol, W.; Bringmann, P.; Alagon, A Gene 105, 229-237, 1991
A; Title: The plasminogen activator family from the salivary gland of the vampire b A; Accession: JSO597; MUID:92039036; PMID:1937019
A; Accession: JSO597; MUID:92039036; PMID:1937019
A; Accession: JSO597; MUID:92039036; PMID:1937019
A; Accession: JSO597; MUID:9166070; PIDN:AAA31591.1; PID:9166071
A; Accession: JSO597
A; Accession: JSO597; MUID:9166070; PIDN:AAA31591.1; PID:9166071
C; Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat homology calcade calc
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                                                   Pred. No. 4.7e-05;
Mismatches 0;
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Jobseph activator (EC 3.4.21.68) beta precursor - common vampire bat
N.Alternate names: tissue plasminogen activator
C;Species: Desmodus rotundus (common vampire bat)
C;Accession: Janar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C;Accession: JS0599
R;Kraetzschmar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A Gene 105, 229-237, 1991
A;Accession: JS0599
A;Accession: JS0699
A;Accession: JS069
A;Accession: JS0699
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                                                                                                                                                                                                                                                                                          Lybour transfer names: tissue plasminogen activator tylosue blasminogen activator (EC 3.4.21.68) gamma precursor - common vampost bat)

C;Species: Desmodus rotundus (common vampire bat)

C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-18. C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-18. C;Accession: JS0600

R;Kraetzschmar, J: Haendler, B: Langer, G: Boidol, W: Bringmann Gene 105, 229-237, 1991

A;Title: The plasminogen activator family from the salivary gland o A;Reference number: JS0697; MUID:92039036; PMID:1937019

A;Reference number: JS0597; MUID:92039036; PMID:1937019

A;Residues: 1-394 <KRA>

A;Residues: 1-394 <KRA>

A;Residues: 1-394 <KRA>

A;Cross-references: GB:M63990; NID:g166078; PIDN:AAA31595.1; PID:g1

A;Note: the authors translated the codon ATC for residue 75 as Thr C;Superfamily: tissue plasminogen activator; EGF homology; fibronec C;Keywords: fibrinolysis; glycoprotein, hydrolase; kringle; serine F;1-21/Domain: signal sequence #status predicted <PIC;Superfamily: tringle homology <RRG>
F;37-394/Product: plasminogen activator gamma #status predicted <PICF;143-388/Domain: trypsin homology <RRG>
F;143-126/Bonmain: trypsin homology <RRG>
F;142-143/Cleavage site: His-Ser (plasmin) #status predicted F;142-143/Cleavage site: His, Asp, Ser #status predicted F;315/Binding site: carbohydrate (Asn) (covalent) #status predicted F;315/Binding site: Garbohydrate (Asn) (covalent)
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Pred. No. 4.4e-05;
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ed. No. 2.9e-05; Mismatches 0;
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C. plasminogen activator (EC 3.4.21.68) precursor - mouse Cipgetels: Mus musculus (house mouse)
C. plate: 10-8ep-1999 #sequence_revision 10-8ep-1999 #text_change 10-8ep-1999
C. plate: 10-8ep-1999 #sequence_revision 10-8ep-1999 #text_change 10-9ep-1999
C. plate: 10-8ep-1999 #sequence_revision 10-8ep-1999 #text_change 10-9ep-1999
R. Micklea, R. J.; Darrow, A. L.; Strickland, S.
J. Biol Chem. 253, 1553-1559, 1988
A. Pittle: Molecular cloning of complementary DNA to mouse tissue plasminogen activator
A. Pittle: Molecular cloning of complementary DNA to mouse tissue plasminogen activator
A. Microsa-reference number: A2941; MUID:88087303; PMID:282648
A. Microsa-reference mulber: A2941; MUID:88087303; PMID:282648
A. Microsa-reference number: A29425
A. Molecula type: more and activator of the murine plasma fibrinolytic system.
A. Reference number: S48205
A. Molecula type: protein
A. Molecula type:
C; Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-29/Domain: propeptide #status predicted <PRO>
F;18-29/Domain: propeptide #status predicted <PRO>
F;30-59/Product: t-plasminogen activator chain A #status predicted <ACH>
F;30-308/Product: t-plasminogen activator chain A #status predicted <ACH>
F;38-75/Domain: EGF homology <EGF>
F;124-205/Domain: EGF homology <EGF>
F;213-294/Domain: kringle homology <KR1>
F;213-294/Domain: kringle homology <KR2>
F;309-553/Domain: trypsin homology <TRY>
F;309-553/Domain: trypsin homology <TRY>
F;309-553/Domain: trypsin homology <TRY>
F;309-553/Domain: trypsin homology <TRY>
F;38-68,66-75,83-94,88-105,107-116,124-205,145-187,176-200,213-294,234-276,265-289,29'
F;38-68,66-75,83-94,88-105,107-116,124-205,145-187,176-200,213-294,234-276,265-289,29'
F;308-309/Cleavage site: Arg-Ile (plasmin, trypsin) #status predicted
F;308-309/Cleavage site: His, Asp, Ser #status predicted
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-
C;Accession: A35029; A31597
R;Feng, P.; Ohlsson, M.; NY, T.
J. Biol. Chem. 265, 2022-2027, 1990
A;Title: The structure of the TATA-less rat tissue-type plasminogen
A;Reference number: A35029; MUID:90130448; PMID:2105315
A;Accession: A35029
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-559 <FEN>
A;Cross-references: GB:M31197; NID:g207429; PIDN:AAA42261.1; PID:g2
R;Ny, T.; Leonardsson, G.; Hsueh, A.J.W.
DNA 7, 671-677, 1988
A;Reterence number: A31597; MUID:89170114; PMID:3148445
A;Accession: A31597
A;Molecule type: mRNA
A;Residues: 1-379, 'K', 381-559 <NYT>
A;Residues: 1-379, 'K', 381-559 <NYT>
C;Superfamily: tissue plasminogen activator; EGF homology; fibronec
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                                                                                   Length 477;
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                                                                                   Score 13; DB 2; Le Pred. No. 5.1e-05; 0; Mismatches 0;
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R; Kraetzschmar, J.;
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                                                                                                                                                                                                                                                               F;127-208/Domain: kringle homology <KR1>
F;215-296/Domain: kringle homology <KR2>
F;311-562/Product: t-plasminogen activator chain B #status experimental <BCH>
F;311-556/Domain: trypsin homology <TRY>
F;311-556/Domain: trypsin homology <TRY>
F;41-71,69-78,86-97,91-108,110-119,127-208,148-190,179-203,215-296,236-278,267-298;152,483/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;219/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;310-311/Cleavage site: Arg-Ile (plasmin, trypsin) #status experimental
F;357,406/Active site: His, Asp #status predicted
F;513/Active site: Ser #status experimental
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N;Alternate names: Hageman factor (activated)
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Apr-1995 #sequence_revision 22-Apr-1995 #text_change 21-Jan-20.
C;Accession: $45281; A61230.
R;Shibuya, Y.; Semba, U.; Okabe, H.; Kambara, T.; Yamamoto, T.
R;Shibuya, Y.; Semba, U.; Okabe, H.; Kambara, T.; Yamamoto, T.
R;Shibuya, Y.; Semba, U.; Okabe, H.; Kambara, T.; Yamamoto, T.
R;Shibuya, Y.; Semba, U.; Okabe, H.; Kambara, T.; Yamamoto, T.
R;Shibuya, Y.; Semba, U.; Okabe, H.; Kambara, T.; Yamamoto, T.
A;Title: Primary structure of bovine Hageman factor (blood coagulation factor A;Reference number: $45281, MUID:94242782; PMID:8186251
A;Residues: 1-593 <8HI->
A;Residues: 1-593 <8HI->
A;Residues: 1-593 <8HI->
A;Residues: 10-81 <8 Peo.
A;Rores-references: GB:870164
A;Rores-references: GB:870164
A;Rores-references: GB:870164
A;Rores-references: GB:870164
A;Rores-references: GB:870164
A;Residues: 10-167 residue 503 as Phe, GTG for residue 247 as Leu, CCG for residue Crossion and characterization of bovine factor XII (Hageman fact A;Reference number: A61329; MUID:77182112; PMID:861210
A;Rolecule type: protein
A;Rolecule type: protein
A;Residues: 10-16, 'Y', '18-19;525-550 <FUJ>C;Superfamily: coagulation; fibrinolysis; glycoprotein; hydrolase; mono F;88-120/Domain: Eibronectin type I repeat homology <FB:>F;357-587/Domain: Eibronectin type I repeat homology <RGF>F;357-887/Domain: Eibronectin type I repeat homology <RRS>F;350-587/Domain: Eibronectin type I repeat homology <RRS>F;351-87/Domain: Eibronectin
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Acta 1159, 113-121, 1992
tructure of guinea-pig Hageman factor: sequenc
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S28941
Coagulation factor XIIa (EC 3.4.21.38) - guinea pig (frag
Coagulation factor
N; Alternate names: Hageman factor
C; Species: Cavia porcellus (guinea pig)
C; Date: 25-Feb-1994 #sequence_revision 03-Aug-1995 #text_
C; Accession: S28941
R; Semba, U.; Yamamoto, T.; Kunisada, T.; Shibuya, Y.; Tan
Biochim. Biophys. Acta 1159, 113-121, 1992
A; Title: Primary structure of guinea-pig Hageman factor:
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6.2e-05;
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Pred. No. 6.20
0; Mismatches
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Nithernate manages ingequence revision 30-701-191 #text change 08-Dec-2000 Cispeciaes Homo sapiens (man) Cispeciaes: Homo sapiens (man) Ricoll, DE: MacGillivary, R.T.A.

Airlite: Characterization of the human blood coagulation factor XII gene. Intron/exon Airlite: Characterization of the human blood coagulation factor XII gene. Intron/exon Airlite: Characterization of the human coagulation factor XII gene. Intron/exon Airlite: Characterization of the human coagulation factor XII (Hageman).

Airlite: Characterization of human coagulation factor XII (Hageman).

Airlite: Characterization of human blood coagulation factor XII (Hageman).

Airlite: Characterization of human blood coagulation factor XII (Characterization of human blood coagulation factor XII (Characterization of human blood coagulation factor XII (Hageman).

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Airlite: Characterization of human blood coagulation factor XII (Hageman factor).

Airlite: Characterization of human blood coagulation factor XII (Hageman factor).

Airlite: Characterization of human blood coagulation factor XII (Hageman factor).

Airlite: Characterization of a cDNA coding for human factor XII (Hageman factor).

Airlite: Characterization of a cDNA coding for human factor XII (Hageman factor).

Airlite: Characterization of a cDNA coding for human factor XII (Hageman factor).

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A; Reference number: $28941; MUID: 93003367; PMID: 1390917
A; Accession: $28941
A; Accession: $28941
A; Status: preliminary
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-603 <SEM>
A; Residues: 1-603 <SEM
A; Residues: 1-60
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Fujikawa, K.; McMullen, B.A.
Biol. Chem. 258, 10924-10933, 1983
Title: Amino acid sequence of human beta-factor XIIa.
Title: Amino acid sequence of human beta-factor XIIa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; LLC.
6.3e-05;
0;
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-May-2000

9

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Stockes

Lyppain-like proteinase (EC 3.4.21.-) precursor - flesh fly (Sarcophaga bullata)
C;Species: Sarcophaga bullata
C;Species: Sarcophaga bullata
C;Species: Sarcophaga bullata
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C;Accession: S5465, S55403
C;Accession: S65465, S55403
A;Reference number: S65403; MulD:96203936; PMID:8620885
A;Residues: 1-254 eBOR>
A;Residues: 1-254 eBOR>
A;Residues: 27-24 eBOR>
A;Residues: 27-36 eBOW>
A;Residues: 27-36 eBOW>
A;Residues: 27-4690; Experimental eBordicted eSRO>
C;Reywords: hydrolase; serine proteinase
F;1-16/Domain: signal sequence #status predicted eSRO>
F;27-24/Domain: trypsin #status experimental eMAT>
F;27-24/Domain: trypsin homology eTRY>
F;27-24/Domain: trypsin head: EBOR eTRY>
F;27-24/Domain: trypsin homology eTRY>
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                                          Complement factor D (BC 3.4.21.46) - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 19.
C;Accession: S54115
R;Nicolas, N.
Submitted to the EMBL Data Library, April 1995
A;Reference number: S54115
A;Accession: S54115
A;Accession: S54115
A;Catus: preliminary
A;Accession: S54115
A;Estus: preliminary
A;Cross-references: EMBL:Z49058; NID:g773264; PIDN:CAA88844.1; PID
C;Superfamily: trypsin; trypsin homology
C;Keywords: complement alternate pathway; hydrolase; plasma; sering
F;1-181/Domain: trypsin homology (fragment) <TRY>
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A,Accession: A21037
A,Molecule type: protein
A,Robicsule type: protein
A,Robicsule type: protein
A,Residues: 354-362,373-615 cFUJ>
B,Harris, R. J.; Ling, V. T.; Spellman, M.W.
J. Biol. Chem. 267, 5102-5107, 1992
A,Title: O-linked fucose is present in the first epidermal growth factor domain of farefarence number: A46605, MUID:92184750; PMID:1544894
A,Contents: amnotation; carbohydrate binding site
C,Genetics:
A,Genetics:
A,Genetics:
A,Genetics: A,Genetics:
A,Complex: factor XII, prekallikrein, and HWM kininogen form a complex bound to anic
C,Function: 19/3; 39/1; 72/2; 96/1; 113/1; 117/1; 212/1; 267/2; 340/1; 417/2; 463/1;
C;Complex: factor XII, prekallikrein, and HWM kininogen form a complex bound to anic
C,Function: factor XII catalyzes the proteolytic activation of plasminogen, plas
ikrein
A,Description: factor XII catalyzes the proteolytic activation of plasminogen, plas
ikrein
A,Pathway: blood coagulation; fibrinolysis; glycoprotein; hydrolase; kringle plasm
C,Superfamily: caagulation; fibrinolysis; glycoprotein; hydrolase; kringle plasm
F,1-13/Domain: signal sequence #stetus predicted 'SIG>
F,20-372,373-615/Product: caagulation factor XIIa, alpha form #status experimental 'F,47-88/Domain: fibronectin type I repeat homology 'FEZ>
F,17-296/Domain: fibronectin type I repeat homology 'AFEZ>
F,17-296/Domain: fibrone
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C; Species: Xenopus laevis (African clawed frog)
C; Species: Xenopus laevis (African clawed frog)
C; Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change
C; Accession: T30337
R; Yang, J.C.; Lindsay, L.L.; Hedrick, J.L.
submitted to the EMBL Data Library, March 1998
A; Description: cDNA cloning of ovochymase, a chymotrypsin-like p
A; Reference number: Z20829
A; Reference number: Z20829
A; Accession: T30337
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-1524 < YAN>
A; Cross-references: EMBL: U81290; NID: g2981640; PIC
C; Superfamily: tryosin related polyprotein; trypsin homology
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ALIGNMENTS

Human; KLK-L1; KLK-L2; KLK-L3; KLK-L4; KLK-L5; KLK-L6; kallikrein-like protein; serine protease; cytostatic; cancer; 248 AA 99US-0124260P. 99US-0127386P. 99US-0144919P. 2000WO-CA000258 SINAI HOSPITAL AAB21304 standard; protein; entry) Diamandis EP; #4 Human KLK-L5 protein (first WPI; 2000-587440/55 prostrate cancer WO200053776-A2 (MOUN) MOUNT 11-MAR-1999; 01-APR-1999; 21-JUL-1999; 09-MAR-2000; Homo sapiens 14-SEP-2000. 02-FEB-2001 GM, AAB21304; Yousef RESULT 1

(KLK-L) proteins for diagnosing orders, especially cancer. New kallikrein-like (KLK-L) protein mediated disorders, N-PSDB; AAA95944

and treating KLK-L

The present sequence is one of four alternatively spliced kallikrein-like proteins encoded by the human KLK-L4 gene. Kallikreins and kallikrein-like proteins are a subgroup of the serine protease enzyme family. They catalyse the selective cleavage of specific polypeptide precursors to release peptides with potent biological activity. Nucleic acids encoding kallikrein-like proteins KLK-L1, KLK-L2, KLK-L3, KLK-L4, KLK-L5 and KLK-L6 have been isolated. The proteins are useful in the treatment, monitoring and diagnosis of cancers, especially prostrate cancer. They can also be used to identify a substance that can associate with or mediate the biological activity of the proteins. Antibodies can be used Claim 12; Page 172; 184pp; English

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Ashkenazi AJ, Baker Ki
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                                                                                                                                                                                                                                                                                  Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation; diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy; angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic; cytostatic; gene therapy; vaccine.
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                                                                                                                                            TSNMVCAGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDW
                                                                 TSSVOPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI
                                                                                                                         TSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI
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                                                         CVLGLSQAATPKI FNGTECGRNSQPWQVGL
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Pred. No. 8.4
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98US-0112850P.

99WS-0115554P.

99WS-0123957P.

99US-0131445P.

99US-0134287P.

99WS-0134287P.

99WS-0141037P.

99WS-0144758P.

99WS-0144758P.

99WO-US020594.

99WO-US020594.

99WO-US021090.

99WO-US021647.
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conditions
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16-DEC-1998;
12-JAN-1999;
08-MAR-1999;
28-APR-1999;
02-JUN-1999;
23-JUN-1999;
26-JUL-1999;
26-JUL-1999;
26-JUL-1999;
13-SEP-1999;
13-SEP-1999;
15-SEP-1999;
15-SEP-1999;
15-SEP-1999;
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The present invention describes nucleic acids encoding PRO polypeptides

useful for preventing, diagnosing and treating diagnosing a

cardiovascular, endothelial or angiogenic disorder in mammals by

modulating cell proliferation, angiogenesis and cardiovascularisation,

and for identifying agonists and antagonists of these processes. The

nucleic acids and the proteins they encode may be used in the prevention,

treatment and diagnosis of diseases associated with inappropriate PRO

expression such as cardiovascular, endothelial or angiogenic disorders in

mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For

example, the nucleic acids (NCs) and vectors containing them and the PRO

polypeptide may be used to treat disorders associated with decreased PRO

expression. AAA77510 to AAA77721 and AAB24388 to AAB24435 represent

nucleotide and protein sequences used in the exemplification of the
                                                                                                                                                                                Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorders in mammals.
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    Hillan KJ;
Kuo SS, F
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100.0%; Pred. No. 8.4e-182;
iive 0; Mismatches 0;
Gerber H,
Klein RD,
Wood WI;
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 , Ferrara N, Gurney AL, Williams PM,
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Best Local Similarity 100.
Matches 248; Conservative
    Baker KP,
dowski PJ,
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diagnosis; screening

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membrane bound protein; receptor;
i, immunoadhesion; pharmaceutical;
                acid
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98US-0098843P.
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98US-0099536P.
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98US-0099642P.
98US-0099642P.
98US-0099741P.
98US-0099783P.
98US-0100684P.
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98US-0100474P.
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98US-0101473P.
98US-010133P.
98US-010133P.
98US-0101330P.
98US-0102330P.
98US-0102330P.
98US-0102331P.
98US-0102331P.
                                                polypeptide; mane; secretion;
                 (0NO669)
                                                                transmembrane;
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                Human PRO1303
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01-SEP-1998;

02-SEP-1998;

02-SEP-1998;

02-SEP-1998;

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04-SEP-1998;

05-SEP-1998;

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115-SEP-1998;

116-SEP-1998;

117-SEP-1998;

118-SEP-1998;

118-S
                                                                                                                                                                09-MAR-2000
                                                PRO
                                                Human;
The present invention describes an antibody that binds to a human protein (I) selected from: PRO381; PRO1269; PRO1303; PRO1755; PRO1780; PRO4334; PRO4927; PRO1557; PRO1295; PRO1203; PRO4304; PRO4354; PRO4397; PRO1927; PRO1555; PRO1096; PRO2038; and PRO2662. (I) has anticancer activity and can be used to diagnose tumours in mammals, by detecting complex formation when the antibody is contacted with test cells. Increased expression of genes encoding (I) can also be detected to diagnose tumours. Agents which inhibit the activity of (I), especially the antibodies, or an antisense oligonucleotide which hybridises to genes encoding (I), can be used to inhibit tumour growth, preferably by inducing cell death. Methods from the present invention can be used to inhibit the biological activity of (I). AAC58019 to AAC58102 represent PCR primers and hybridisation probes used in examples from the present invention for human PRO sequences. AAC58103 to AAC58122 and AAB24021 to AAB24040 represent human PRO polymucleotide and protein sequences given in the exemplification of the present invention
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                                                                                                                                                                                                                                                                 for PRO polypeptides, used to diagnose is in mammals, and to identify inhibitors or expression.
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polypeptide activity or
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N-PSDB; AAC58114.
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01-DEC-1999;
                  02-DEC-1999;
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30-SEP-1998;
01-OCT-1998;
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biodiversity;
                                     AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding then have various industrial applications, including uses as pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR primers and hybridisation probes used in the isolation of the PRO polypeptides from the present invention
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larity 100.0%; Pred. No. 8.4e-182;
Conservative 0; Mismatches 0;
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inhibitors of the
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248; Conser
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17-JUL-2000;
03-AUG-2000;
15-SEP-2000;
                   Fig
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05-JAN-2000;
06-JAN-2000;
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useful as
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                            raising
                                                proteins from a variety of organisms, including human, dog, cat, ho cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present server
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Pred. No. 8.4
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99US-0144758P.
99US-0145698P.
99WO-US020111.
99WO-US028313.
99WO-US028551.
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                                   research us
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                           Isolated polypeptide antibodies and resear
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      01-476164/51
AAH98653.
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20-JUL-1999;
26-JUL-1999;
01-SEP-1999;
29-OCT-1999;
30-NOV-1999;
02-DEC-1999;
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                                                                                                                                                                                                                                                                                             and nucleic acids designated PRO, chromosome and gene mapping and gene
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                                                                                                                     Fong S;
Hillan KJ;
Watanabe (
                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to secreted and transmembrane proteins. These proteins and the DNA encoding them may be used as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. They may also be used used to generate either transgenic animals or knockout animals which are in turn useful for development and screening of therapeutically useful reagents. The nuclacids may also be used in gene therapy
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naldi CJ, Gu
Stewart TA,
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Gao W, Goddard A, Godowski PJ, Grimaldi C
Pan J, Paoni NF, Roy MA, Smith V, Stewar
Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                           ed and transmembrane proteins as hybridization probes, in c
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2000WO-US000376
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98US-0106032P

98US-0106033P

98US-010603P

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98US-0108867P

98US-01088
06-OCT-1998;

07-OCT-1998;

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22-OCT-1998;

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27
    arthritis
      injury;
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98US-0098723P.
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98US-0098723P.
98US-0098750P.
98US-0098803P.
98US-0098812P.
98US-0098843P.
98US-0098843P.
98US-0099536P.
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98US-0099754P.
98US-0100684P.
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98US-0102540P.
98US-0102540P.
98US-0102540P.
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antidiabetic; anorectic; antiarthritic; angiogenesis; cancer; adrenal cortical capillary; endothelial cell growth; wound healing; stimulated T-lymphocyte proliferation; immune response suppression; neonatal heart hypertrophy; cardiac insufficiency disorder; vascular endothelial growth factor; inflammation; mononuclear cell; eosinophil; diabetes; obesity; or hyper-insulinaemia; hypo-insulinaemia; chondrocyte redifferentiation; bone disorder; cartilage disorder; sports injury; arthritis.
                                                                                                                                                                                                                                                                                            98US-0098716P.
98US-0098723P.
98US-0098723P.
98US-0098750P.
98US-0098843P.
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skeletal
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PRO1787 that modulate glucose or free fatty acid uptake by
muscle cells, and are useful for treating diabetes, hyper-
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A, Tumas D
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Williams PM, Woo
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Fong S;
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Gurney AL,
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MA, Smith
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Williams PM, Wood WI;
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98US-0099764P.
98US-0099764P.
98US-0099816P.
98US-0099816P.
98US-0099816P.
98US-0100388P.
98US-0100381P.
98US-0100684P.
98US-0101071P.
98US-0101471P.
98US-0101474P.
                                                                                                                                                                                                                                                             2001US-00013907
                                                                                         ADC18063 standard; protein;
                                                                                                                                 (first entry)
                                                                                                                                                   Human PRO polypeptide #54
                      248
                                         248
                                                                                                                                                                       PRO; protein
                                  IRMIMRNN
                       IRMIMRNN
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23-SEP-1998;
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                                                                                                             ADC18063;
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                      241
                                                                                                                                                                                 genetic
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ADC1806
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Hillan KJ;
Watanabe CK;
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Surney AL,
Tumas D,
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\STSHEHDL
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Grimaldi JC, Gu
IV, Stewart TA,
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Pred. No. 8.4e-182;
Mismatches 0;
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99US-00284291.
99US-01129674P.
99US-0141037P.
99US-0144758P.
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99WO-US028313.
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99WO-US03841.
2000WO-US00376.
2000WO-US003565.
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2000WO-US003565.
2000WO-US014042.
2000WO-US014042.
2000WO-US014941.
2000WO-US013705.
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2000WO-US013666.
2001WO-US03666.
2001WO-US036666.
2001WO-US03692.
2001WO-US01785.
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Best Local Similarity 100.0%;
Matches 248; Conservative
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                                                                                                                                                                                                                                                                                                                                                               GENENTECH INC
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N-PSDB; ACD68024.
12-APR-1999;
23-JUN-1999;
20-JUL-1999;
26-JUL-1999;
01-SEP-1999;
15-SEP-1999;
02-JUK-1999;
02-JUK-1999;
05-JAN-2000;
06-JAN-2000;
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02-MAR-2000;
17-MAY-2000;
24-FEB-2000;
24-FEB-2000;
02-MAY-2000;
02-JUN-2000;
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04-MOY-2000;
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01-JUN-2001;
14-JUN-2001;
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29-JUN-2001;
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98US-0101915P.

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98US-0102240P.

98US-0102331P.

98US-0102331P.

98US-0105687P.

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98US-0105687P.

98US-0105683P.

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98US-0106032P.

98US-0106033P.

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   23-SEP-1998;
24-SEP-1998;
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25-SEP-1998;
26-SEP-1998;
27-OCT-1998;
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Fong S;
Hillan KJ;
Watanabe CK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to human PRO polypeptides and the polynucleotides encoding them. The sequences are useful in the preparation of a medicament for treating a condition responsive to a PRO polypeptide. The polypeptides are useful in a number of functional biological assays, as molecular weight markers for protein electrophoresis and as therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . PRO1491 and PRO1571, useful in the ating a condition responsive to PRO nts e.g. vaccines.
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Gurney AL,
A, Tumas D,
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8.4e-182;
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Grimaldi JC,
V, Stewart TA
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treating a a
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Pred. No. 8.4
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Goddard A, Godowski PJ,
Paoni NF, Roy MA, Smith
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98US-0108851P.
98US-0108852P.
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98US-0108858P.
98US-0108904P.
98US-0113296P.
98US-0113296P.
98US-0114223P.
98US-0114223P.
98US-0114223P.
99US-0114223P.
99US-0144758P.
99US-014941.
2000WO-US013705.
2000WO-US013705.
2000WO-US013705.
2000WO-US013705.
2000WO-US033328.
2000WO-US03332678.
2000WO-US03332678.
2001WO-US030873.
2001WO-US019692.
2001WO-US01735.
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Best Local Similarity 100.0%;
Matches 248; Conservative
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WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 12; SEQ ID NO 194;
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N-PSDB; ADC18062.
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18-NOV-1998;

18-NOV-1998;

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27-MAY-2000;

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28-FEB-2000;

29-MAY-2000;

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22-MAY-2000;

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23-AUG-2000;

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flux;
disorder;
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eliac disease;
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Human; secreted protein; transmembrane protein; PRO; tumou immune response; cardiac insufficiency disorder; calcium fumbilical vein endothelial cell; bone disorder; cartilage arthritis; wound healing; diabetes; skeletal muscle cells; Berger disease; nephropathy; Schonlein-Henoch purpura; coedermatitis; herpetiformis; Crohn's disease; thalassaemia.
                           FPDLLQ
                                    secreted/transmembrane protein PRO1303
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98US-0100388P.
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Human, secreted protein, transmembrane protein, PRO, tumour, immune response, cardiac insufficiency disorder; calcium flux, umbilical vein endothelial cell, bone disorder; cartilage disorder, arthritis, wound healing, diabetes; skeletal muscle cells, obesity; Berger disease, nephropathy; Schonlein-Henoch purpura; coeliac disease, dermatitis; herpetiformis; Crohn's disease; thalassaemia.
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  / Match 100.0%;
Local Similarity 100.0%;
les 248; Conservative (
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18-FEB-2000;

17-MAY-2000;

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10-NOV-2000;

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Best Local S
Matches 248
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ADD3978
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ÇĶ;
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Hillan KJ;
Watanabe C
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Gurney AL,
A, Tumas D,
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Grimaldi JC,
V, Stewart T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     isolated PRO
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Godowski PJ, (
Roy MA, Smith '
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98US-0108775P.
98US-0108775P.
98US-0108775P.
98US-0108775P.
98US-010878P.
98US-010878P.
98US-0108801P.
98US-0108801P.
98US-0108801P.
98US-0108802P.
98US-0108802P.
98US-0108802P.
98US-0108802P.
98US-0108804P.
98US-0108867P.
98US-0108867P.
98US-0108868P.
99US-0113296P.
99US-0113296P.
99US-0113296P.
99US-0113296P.
99US-0108888P.
99US-0108904P.
99US-0113296P.
99US-0113296P.
99US-0113296P.
98US-0108904P.
99US-0113296P.
99US-0108904P.
99US-0113296P.
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Goddard A, (
Paoni NF, Ro
s PM, Wood WI
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N-PSDB; ADD70708.
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 10-NOV-1998;

17-NOV-1998;

18-NOV-1999;

22-DEC-1999;

22-DEC-1999;

23-JUN-1999;

24-NOV-1999;

25-DEC-1999;

25-DEC-1999;

26-JUL-1999;

26-JUL-1999;

27-NOV-1999;

28-NOV-1999;

29-OCT-1999;

20-JUN-1999;

21-NOV-1999;

22-DEC-1999;

22-DEC-1999;

23-JUN-1999;

24-AUG-2000;

24-AUG-2000;

24-AUG-2000;

24-AUG-2000;

26-JUN-2000;

26-JUN-2000;

27-MAY-2000;

28-NAY-2000;

29-OCT-1999;

20-JUN-2000;

21-MAY-2000;

21-MAY-2000;

22-MAY-2000;

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PRO1787
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98US-0098723P.
98US-0098749P.
98US-0098750P.
98US-0098821P.
98US-0098843P.
98US-0099536P.
98US-0099536P.
98US-0099536P.
98US-0099536P.
98US-0099754P.
98US-0099754P.
98US-0099763P.
98US-0099763P.
98US-0099763P.
98US-0099815P.
98US-0100388P.
98US-0100388P.
98US-0100388P.
98US-0100584P.
98US-0100661P.
98US-0100661P.
98US-0100664P.
98US-0100664P.
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98US-0100919P.
98US-0100930P.
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98US-0101014P.
98US-0101068P.
98US-0101071P.
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                                                                                                                            standard; protein;
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                                      IRMIMRNN
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                                        241
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                181
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                                                                                                    RESULT 13
                                                                                                              ADD702
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                                                                                                                                                                                                                                                                                   The invention relates to an isolated PRO polypeptide (secreted or transmembrane protein) having at least 80% amino acid sequence identity to an amino acid sequence and come and acid sequence acid sequence as given in the specification (including their extracellular domains either or without their associated signal peptides. Also include are the nucleotide (NA) sequences encoding PRO, a vector comprising the PRO NA, a host cell comprising the vector, producing PRO, a chimaeric molecule comprising PRO fused to a heterologous amino acid sequence, and an antiporation professing and also for chromosome identification. PRO is also useful for tissue typing. PRO and PRO NA are useful as hybridisation probase for a CDNA library to isolate the full-length PRO CDNA. PRO NA is useful for generating transgenic animals or knock-cut animals which are useful in development and screening useful reagents. PRO NA is useful in development and screening useful reagents. PRO NA is useful in development for suppressing immune response. PRO1246 and pRO1410 polypeptides are useful for reating cardiac insufficiency disorders. PRO1266 polypeptide are useful for suppressing immune response. PRO1246 and PRO146 polypeptide are useful for treating calcium flux in human prolypeptides are useful for treating calcium flux in human collical wain endothelial cells. PRO1265, PRO1265 and PRO1418 polypeptides are useful for treating bone and/or cartiage disorders (e.g., arthritis) and wound healing. PRO130, PRO1265 and PRO1418 polypeptides are useful for treating bone and/or cartiage disorders (e.g., arthritis) and wound healing. PRO130, PRO1265, PRO1265, PRO1265, PRO1265, PRO1265, PRO1265, PRO1265, PRO1304, PRO1365, PRO1365, PRO1365, PRO1265, PRO1365, PRO1304, PRO1366, PRO1418 propermer PRO1418 are useful in treating that assembles are useful for treating that secure of the invention. The present sequence represents a PRO Protein of the invention.
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                                                                                                              Fong S;
Hillan KJ;
Watanabe C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTA
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Ltus, hyper-
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                                                                                                                                                                                                               New secreted and transmembrane PRO polypeptides useful for cancers, kidney disorders, Crohn's disease, diabetes mellithypo-insulinemia, sports injuries and arthritis.
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                                                                                                                Ferrara N
                                                                                                                                        Tumas D
                                                                                                                            Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; DB 7; L
8.4e-182;
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                                                                                                               Eaton DL,
                                                                                                        Botstein D, Desnoyers L, Eaton DL, Idard A, Godowski PJ, Grimaldi JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 248; 1
100.0%; Pred. No. 8.
                                                                                                                                                                                                                                                                  ID NO 194; 557pp; English
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 2001WO-US006666.
2001WO-US017800.
2001WO-US019692.
2001WO-US021066.
2001WO-US021735.
2001US-00946374.
                                                                                                                                     NF, Roy MA,
Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                       GENENTECH INC.
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N-PSDB; ADD39785.
                                                                                                                          Goddard A,
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248; Conser
                                                                                                                                    Paoni NF,
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01-MAR-2001;
01-JUN-2001;
20-JUN-2001;
29-JUN-2001;
                                                 09-JUL-2001;
                                                                                                                                                    Williams PM,
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                                                                                                                Baker KP
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Pan J,
                                                                                       (GETH )
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Human secreted/transmembrane protein PRO1303
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98US-0101471P.
98US-0101472P.
98US-0101472P.
98US-0101475P.
98US-0101477P.
98US-0101477P.
98US-0101477P.
98US-0101477P.
98US-0101477P.
98US-0101473P.
98US-0101741P.
98US-01017783P.
98US-01017783P.
98US-01017783P.
98US-01017783P.
98US-01017783P.
98US-01017783P.
98US-01017783P.
98US-01017788P.
23-SEP-1998;
23-SEP-1998;
23-SEP-1998;
23-SEP-1998;
23-SEP-1998;
23-SEP-1998;
24-SEP-1998;
25-OCT-1998;
27-OCT-1998;
27-OC
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Fong S;
Hillan KJ;
Watanabe CK;
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in protein
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Gurney AL,
A, Tumas C
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markers
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8.4e-182;
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Grimaldi JC,
V, Stewart TA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match
Local Similarity 100.0%; Score 248; 1
Local Similarity 100.0%; Pred. No. 8.4
Les 248; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated PRO
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Gao W, Goddard A, Godowski PJ,
Pan J, Paoni NF, Roy MA, Smith
Williams PM, Wood WI;
98US-0108807P.
98US-0108867P.
98US-0108867P.
98US-0108848P.
98US-0108849P.
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98US-0113296P.
98US-0113296P.
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98US-0113296P.
98US-0113296P.
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99US-01089511.
99US-0114223P.
99US-01144758P.
99US-0108858P.
99US-0114223P.
99US-0114223P.
99US-01189692.
2001WO-US013652.
2001WO-US013692.
2001WO-US01352.
2001WO-US01352.
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N-PSDB; ADD70231.
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17-NOV-1998;
17-NOV-1998;
18-NOV-1998;
18-NOV-1998;
18-NOV-1998;
18-NOV-1998;
18-NOV-1998;
22-DEC-1999;
23-JUN-1999;
24-FEB-2000;
25-JAN-2000;
25-JAN-2000;
25-JAN-2000;
15-SEP-1999;
26-JUL-1999;
26-JUN-1999;
27-DEC-1999;
28-JEB-2000;
28-JAN-2000;
28-JAN-2000;
28-JAN-2000;
28-JAN-2000;
28-JAN-2000;
29-JUN-2000;
21-MAY-2000;
23-AUG-2000;
23-AUG-2000;
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26-JUN-2001;
29-JUN-2001;
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29-JUN-2001;
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98US-0100849P.
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98US-0101071P.
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98US-0102687P.
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Human; secreted protein; transmembrane protein; PRO; tumour; immune response; cardiac insufficiency disorder; calcium flux; umbilical vein endothelial cell; bone disorder; cartilage disorder; arthritis; wound healing; diabetes; skeletal muscle cells; obesity; Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease; dermatitis; herpetiformis; Crohn's disease; thalassaemia.
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transmembrane protein) having at least 80% amino acid sequence identity
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98US-010878P.
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, Goddard A, Godowski PJ, Grimaldi JC,
, Paoni NF, Roy MA, Smith V, Stewart ' NF, Roy Wood WI; Pan J, Paoni Williams PM, Baker Gao W,

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Adams M., Mural R.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ datab.
EMBL; AY152434; AAN78422.1; -.
MGD; MGI:2447533; K1k15.
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR009003; Cys Ser_trypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
Pfam; PF00089; trypsin; 1.
PROSITE; PS00134; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                          ..4e-52;
nes 93;
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                    DB
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Pred. No. 1e-50;
30; Mismatches
                  Score 627.5;
Pred. No. 1.4e
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=22325484; PubMed=12437987, Olsson A.Y., Lundwall A.; "Organization and evolution of the musculus."; Biochem. Biophys. Res. Commun. 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30;
                                       24;
                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 23, (TrEMBLrel. 23, 1) (TrEMBLrel. 25, 1)
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larity 49.0%;
Conservative 3
                Query Match
Best Local Similarity 50.2%;
Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                            245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheri
NCBI_TaxID=10090;
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|KK||:
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01-MAR-2003
01-OCT-2003
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QBCGR4;
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Best Loc
Matches
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ID Q
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Catarrhini; Hominidae;
                                                                         IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
        MEROPS; S01.020; -.
MEROPS; S01.020; -.
MGD; MGI:1916761; 231000BB01Rik.
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0004295; F:peptidase activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IE.
InterPro; IPR009003; Cys Ser trypsin.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase S1.
InterPro; IPR001314; Peptidase S1A.
PRINTS; PR00722; CHYMOTRYPSIN.
                                                                                                                                                                                                                                             11;
                                                                                                                                                                                                                                                         44;
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                                                                                                                                                                                                                                           Score 952.5; DB Pred. No. 4.1e-847; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260
                                                                                                                                    SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Protease; Serine protease.
NON_TER
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Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1
PROSITE; PS00134; TRYPSIN_HIS; 1
PROSITE; PS00135; TRYPSIN_HIS; 1
Hypothetical protein.
SEQUENCE 260 AA; 28090 MW; E
                                                                                                                                                                                                                                                                 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , Metazoa; Chordata;
Eutheria; Primates;
                                                                                                                                                                                                                   25888 MW;
                                                                                                                                                                                                                                          69.3%;
llarity 70.6%;
Conservative 2
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23,
25,
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(TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
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Strausberg R.;
Submitted (DEC-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Human)
                                                                                                                                                                                                                                        Query Matcn
Best Local Similarity
Matches 166; Conser
                                                                                                                                                                                                                   234 AA;
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Ецкагуота; Ме
Маттаlia; Eut
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01-MAR-2003
01-OCT-2003
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Prints; Pr00089; trypsin; 1.

PRINTS; PR00722; CHYMOTRYPSIN.

SMART; SM00020; Tryp SPC; 1.

PROSITE; PS50240; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN HIS; 1.

PROSITE; PS00135; TRYPSIN SER; 1.

SEQUENCE 249 AA; 27604 MW; F.
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larity 47.0%;
Conservative 3
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13,
25,
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(TrEMBLrel.
(TrEMBLrel.
                                                                                                                                                                            PRELIMINARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE=Brain;
Yamaguchi N., Mitsui S
Submitted (JUL-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 238 VDWIRMIMRNN
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Best Local Similarity
Matches 118; Conser
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SEQUENCE FROM N.A.
TISSUE=Brain;
                                                                                                                                                                                                   Q9QYN4;
01-MAY-2000
01-MAY-2000
01-OCT-2003
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PRSS20.
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Q9QYN3
ID Q9
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Q9QYN4
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; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30;
                    CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLL
                                               CHGVYPGRITSNMVCA---GGVPGQDACQGDSGGPLVCGGVLQGLVSWGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      275;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nakamura T., Mitsui S., Miki T., Yamaguchi N.;
Nakamura T., Mitsui S., Miki T., Yamaguchi N.;
"Molecular cloning and expression of a variant form of hippostasin/KLK11 in prostate.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ database:
EMBL; AB078780; BAC54105.1;
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR009003; Cys Ser trypsin.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEAM; PF00089; trypsin; 1.

PRINTS; PR00722; CHYMOTRYPSIN.

SMART; SM00020; Tryp_SPc; 1.

PROSITE; PS50240; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_HIS; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

SEQUENCE 275 AA; 30165 MW; 257A42B28F40E2C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            form of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vertebrata; F. Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 23, Created)
(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88;
88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 601; DB 4;
Pred. No. 5.5e-50
5; Mismatches 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           275 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Ve
Mammalia; Eutheria; Primates; Catarrhini;
NCBI_TaxID=9606;
                                                                                                                     SVOPLPLPNDCATAGTECHVSGWGITNHPRNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Variant form hippostasin/KLK11.
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Best Local Similarity 44.2%;
Matches 121; Conservative 3
                                                                                                                                                                                                                                                                                                                            241
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GVYTKVCSYLEWI
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SEQUENCE FROM N.A.
TISSUE=Prostate;
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01-MAR-2003
01-OCT-2003
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Q81XD7
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MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 AHCRKPHYVILLGEHNLEKTDGCEQRRMATESFPHPDFNNSLPNKDHRNDIMLVKMSSPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGA--STSHEHDLRLLRLRLPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 RITSNMVCAG-GVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKX
                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mitsui S., Yamagushi N.;

Mitsui S., Yamagushi N.;

"cDNA cloning of a novel brain serine protease, Hippostasin.";

Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AB016226; BAA88825.1; -.

HSSP; P00763; 1DPO.

MEROPS; S01.257; -.

MGD; MGI:1929977; Prss20.

GO; GO:0005576; C:extracellular; IDA.

InterPro; IPR009003; Cys_Ser_trypsin.

InterPro; IPR001254; Peptidase_S1.

InterPro; IPR001314; Peptidase_S1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           databases
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                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 597.5; DB 11;
Pred. No. 1.1e-49;
3; Mismatches 95;
\boldsymbol{\varpi}
                                           275
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to the EMBL/GenBank/DDBJ
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Q96RQ0
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., Sakai K.,
Shiraki T.,
Tanaka T.,
. Yoshino M.,
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         Q9QXN3;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
11-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hippostasin prostate type (Adult male tongue cDNA, RIKEN full-length enriched library, clone:2310015108 product:protease, serine, 20, full insert sequence) (Adult male tongue cDNA, RIKEN full-length enriched insert sequence)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Tongue;
Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno N.
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
A Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno N.
A Okazaki Y., Okido T., Owa C., Saito H., Sakai C., Sakai I.
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki J.
Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.
Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino A.
Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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Hori F.
                                                                                                                                                                                                                                                                                                                                                           Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       eam;
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STRAIN=C57BL/6J; TISSUE=Tongue;
RIKEN FANTOM Consortium;
"Functional annotation of a full-length mouse cDNA collect
Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murin
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20525460; PubMed=11072088;
Mitsui S., Okui A., Kominami K., Uemura H., Yamagushi N.;
"cDNA cloning and tissue-specific splicing variants of mounippostasin/TLSP (PRSS20).";
hippostasin/TLSP (PRSS20).";
Biochim. Biophys. Acta 1494:206-210(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDN
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Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUB=Tongue;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shiba
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Normalization and subtraction of cap-trapper-selected prepare full-length cDNA libraries for rapid discovery Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S.;
to the EMBL/GenBank/DDBJ
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STRAIN=C57BL/6J; TISSUE=Tongue;
MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA CMeth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Tongue;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Prostate;
Yamaguchi N., Mitsui
Submitted (JUL-1998)
                                                                                                                                                                                                                                                                                                                             musculus (Mouse)
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MEDLINE=20525460;
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Q9QXN3;
01-MAY-2000
01-MAY-2000
01-OCT-2003
                                                                                                                                                                                                                                                              sequence).
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SEQUENCE FROM N.A.

STRAIN=C57BL/60; TISSUE=Tongue;
X MEDINEE-20250913; Pubmed=11076861;
Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Mishine T., Tashiro H., Itoh M., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Samamoto R., Marsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunia S., Kawai J., Okazaki Y., Matsunatsu M., Inoue Y., Kira A., Hayashizaki Y.; RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
TRIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
TRIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary Sl.
TEMBL; AR00950: BAB26241.2;
TREMBL; AR00920: BAB2641.2;
TREMBL; AR00920: BAB26461.2;
TREMBL; AR009003: Cys Ser_trypsin.
TREMPS; DR001224; Peptidase_Sl.
TREMPS; PR001244; Peptidase_Sl.
TREMPS; PR001244; Peptidase_Sl.
TREMPS; PR001254; Peptidase_Sl.
TREMPS; PR001254; TRYPSIN LIS.
TREMPS; PR001254; TRYPSIN LIS.
TREMPS; PR001364; TRYPSIN LIS.
TREMPS; PR001365; TRYPSIN LIS.
TRYPSIN TRYPSIN LIS.
TRYPSIN TRYPS; PR001365; TRYPSIN LIS.
TRYPSIN TRYPS; PR001365; TRYPSIN LIS.
TRYPSIN TRYPS; TRYPSIN LIS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28 MILRLIALALVIGHVGGET-RIIKGYECRPHSQPWQVALFQKTRLLCGATLIAPKWLLTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGA--STSHEHDLRLLRLFLPV
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Last sequence update)
Last annotation update)
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Pred. No. 1.2e-49;
; Mismatches 95;
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MEDLINE=21226193; PubMed=11327827
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Local Similarity 47.0%;
nes 118; Conservative 3
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Homo Bapiens
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Q96RQ0;
01-DEC~2001
01-DEC-2001
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Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Buromstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Leo N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whilttaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Hayashizaki Y.;
Rutcional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
Nature 409:685-690(2001).
SEMBL, AK003996; BAB23113.1;
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
EMBL, AK003996; BAB23113.1;
SEMBL, AK0039996; BAB23113.1;
SEMBL, AK0039996; BAB23113.1;
SEMBL, AK00399999999999999999999999999
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PRINTS; PR00722; CHYMCLALL
SMART; SM00020; Tryp SPC; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
R PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
""Arolase; Protease; Serine protease.
""Arolase; Drotease; Serine protease.
""Arolase; Drotease; Serine protease.
""Arolase; Drotease; Serine protease.
""Arolase; Protease; Serine protease.
""Arolase; Protease; Serine protease.
""Arolase; Protease; Serine protease.
""Arolase; Protease; Serine protease.
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annotation update)
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Pred. No. 9.5e-49;
41; Mismatches 77;
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SEQUENCE FROM N.A.
MEDLINE=22325484; PubMed=12437987
Olbbon A.Y., Lundwall A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptidase_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata;
Rodentia;
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Proceso; trypsin; 1.
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QBCGR6;
01-MAR-2003 (TrEMBLrel. 23, C
01-MAR-2003 (TrEMBLrel. 23, L
01-OCT-2003 (TrEMBLrel. 25, L
Glandular kallikrein KLK13.
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il Similarity 47.2%;
110; Conservative 4
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Mammalia; Eutheria;
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Pfam; PF00
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Matches
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MEDLINE=21085660; PubMed=11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Kadota K., Matsuda H.A., Ashburner M., Petalov S., Cosavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush a
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by
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        T.;
antigen precursor (pro-PSA)
serine protease identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        255
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Sciurognathi; Muridae;
                                                                                                                                                                                          MEROPS; SO1.081; -.

GO; GO:0004263; F:chymotrypsin activity; IEA.

GO; GO:0006295; F:trypsin activity; IEA.

GO; GO:0006508; P:proteolysis and peptidolysis; IEA

InterPro; IPR009003; Cys_Ser_trypsin.

InterPro; IPR001254; Peptidase_S1.

InterPro; IPR001314; Peptidase_S1.

InterPro; IPR001314; Peptidase_S1A.

Pfam; PF00089; trypsin; 1.

PRINTS; PR00722; CHYMOTRYPSIN.

SMART; SM00020; Tryp_SPC; 1.

PROSITE; PS50240; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN DOM; 1.

Hydrolase; Protease; Serine protease.

SEQUENCE 255 AA; 27986 MW; 00D5B79E14B9468F CRC
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43.3%; Score 595; DB 4; larity 46.5%; Pred. No. 1.9e-49 Conservative 32; Mismatches 8
                                                                                                                              S1
                                                                                                                             FAMILY
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                                                                                                 Biochemistry 40:1679-1687(2001).
-!- SIMILARITY: BELONGS TO PEPTIDASE
EMBL; AF303046; AAK62813.1; -.
HSSP; P00761; 1AN1.
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        Takayama T.K., Carter C.A., Deng "Activation of prostate-specific prostin, a novel human prostatic degenerate PCR.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32;
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Mammalia; Eutheria; Rodentia;
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Q9D140;
01-JUN-2001
01-JUN-2001
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MEROPS; S01
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NCBI_TaxID=10090;
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glandular kallikrein
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Sciurognathi; Muridae;
                                                                                                                                                                            IEA
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Last sequence update)
Last annotation update)
                                                                           Adams M., Mural R.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ data EMBL; AY152432; AAN78420.1; -.
EMBL; AY152432; Klk13.
GO; MGI:95292; Klk13.
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IE InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
                                                                                                                                                                                                                                                                                                                                                                  Score 588; DB 11;
Pred. No. 9.9e-49;
3; Migmatches 81;
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                                 299:305-311 (2002)
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                                                                                                                                                                                                                                    Pfam; PF00002; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPC; 1.
PROSITE; PS50240; TRYPSIN DOM; 1
PROSITE; PS00134; TRYPSIN HIS; 1
PROSITE; PS00135; TRYPSIN SER; 1
PROSITE; PS00135; TRYPSIN SER; 1
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Mammalia; Eutheria; Rodentia;
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ilarity 46.3%;
Conservative 3
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Submitted (SEP-2002) to the
EMBL; AY152433; AAN78421.1;
    evolution
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   and
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                  musculus.";
Biochem. Biophys.
                                                               EQUENCE FROM N
                                                                                                                                                                                                                        InterPro; IPRO
Pfam; PF00089;
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    Organization
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Mus musculus
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Sciurognathi; Muridae; Murinae; Mu
                                                                                                                                                                                                                                                                                                                                                                                                                                14;
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1.
F62FEBF2290FEBE8 CRC64;
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Q80VS4;
Q80VS4;
Q80VS4;
Q1-JUN-2003 (TrEMBLrel. 24, Created)
Q1-JUN-2003 (TrEMBLrel. 24, Last sequence update)
Q1-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Q1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Q1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Q1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to kallikrein 14 (Fragment).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae
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STRAIN=NMRI; TISSUE=Breast tumor;
Strausberg R.;
Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ datak
EMBL; BC044756; AAH44756.1; -.
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEI
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
MGD; MGI:2447564; Klk14.

GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0006295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEI
InterPro; IPR00103; Cys Ser_trypsin.
InterPro; IPR001034; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_HIS; 1.
SEQUENCE 250 AA; 27016 WW; F62FEBF2290FEBE8 CR
                                                                                                                                                                                                                                                                                                                                                                            Score 586; DB 11;
Pred. No. 1.4e-48;
0; Mismatches 80;
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PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPc; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
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MEDLINE=22388257; PubMed=12477932;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Villalon D.K., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
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L.J., Hulyk S.W.,
                                                       KIFNGTECGRNSQPWQVGLFEGTSLR--CGGVLIDHRWVLTAAHCSGSRYWVRLGEHSLS
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Length 242
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidi
Xenopodinae; Xenopus.
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Klein S., Strausberg R.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases
EMBL; BC056068; AAH56068.1; ~.
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on update)
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                          75;
DB 11;
 Score 578; DB 11
Pred. No. 7.9e-48
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Last annotation
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               ed. No. 7.96
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MEDLINE=22341132; PubMed=12454917;
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 42.1%;
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TaxID=8355;
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Richardson P.,
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MEDLINE=2388257; Pubmed=12477932;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Yillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W. Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human "Control A.)

"Generation and initial analysis of more than 15,000 full-length human "Control A.)

"The control of the control of 
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Hulyk S.W.,
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Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.
Richardson P.;
"Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                 8;
                                                       Length 248;
                  CRC64;
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Last sequence update)
Last annotation update)
                                                       Score 563; DB 13;
Pred. No. 2.3e-46;
                  1ED9D0D218702860
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Dev. Dyn. 225:384-391(2002)
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                    248 AA;
                                                                            Local Similarity
nes 112; Conser
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Matsui H., Takahashi T.;
Matsui H., Takahashi T.;
"The sequences of mouse serine protease gene expressed in bi Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
EMBL; AB015206; BAA28895.1; -.
EMBL; X18723; CAA77269.1; -.
EMBL; X18723; LDPO.
HSSP; P00763; 1DPO.
MEROPS; S01.236; -.
MGD; MGI:1343166; Prss18.
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"Mouse serine protease preferentially expressed in brain.
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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databases.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, E
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae,
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annotation update)
  99:16899-16903 (2002)
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                                                                                                                                                                                                                                                                                                              C5B82B458B209F31
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STRAIN=BALB/C; TISSUE=Skin;
Meier N., Dear T.N., Boehm T.;
"A novel serine protease expressed in the hair
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ o
                                                                                                                                                 Klein S., Strausberg R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ
EMBL; BC054194; AAH54194.1; -.
Hypothetical protein.
SEQUENCE 243 AA; 25476 MW; C5B82B458B209F
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TISSUE=Brain;
                                                                          SEQUENCE FROM TISSUE=Whole;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Rodentia; Sciurognathi; Murídae; Murinae; Mu
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27496 MW; E20C080087139B63 CRC64;
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Last sequence update)
Last annotation update)
18).
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IE
InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
PRINTS; PR00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_HIS; 1.
Hydrolase; Protease; Serine protease.
SEQUENCE 246 AA; 27496 MW; E20C080087139B63 CR
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Mitsui S., Yamaguchi N.;
"cDNA cloning and characterization of mouse brain
"cDNA cloning and characterization of mouse brain
protease, Neurosin.";
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Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ da
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
EMBL; AB008928; BAB55605.1; -.
EMBL; BC031119; AAH31119.1; -.
HSSP; P00761; 1AN1.
MEROPS; S01.236; -.
MGD; MGI:1343166; Prss18.
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
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                                         GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Protease; Serine protease.
SEQUENCE 253 AA; 28329 MW; C5EF98C7EEF2FBC1 CRC64;
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Best Local Similarity 43.5%; Pred. No. 2e-45;
Matches 107; Conservative 46; Mismatches 8
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248

.. GVYTYICKYVDWIRMIMRNN

MGLSIFLLLCVLGLSQAATP US-10-006-856A-194 BLOSUM62 Gapop 10.0 , score: Sequence: Title: Perfect

Scoring table:

52070155 residues 141681 seqs, Searched:

Gapext 0,

141681 hits satisfying chosen parameters: ΟĘ Total number

length: 0 length: 2000000000 seq seq Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database

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SUMMARIES

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	ID	KLKC_HUMAN	KLK8_HUMAN	NRPN MOUSE	NRPN RAT	KLKB HUMAN	KLKF HUMAN	TRY3_CHICK	KLKE HUMAN	KLK9 HUMAN	KLKD HUMAN		TRY1_CHICK	KLK5 HUMAN	KLKA_HUMAN	TRY2_XENLA		1 1	KLK6_HUMAN	TRY1 XENLA	KLK7_HUMAN	TRY2_MOUSE		ျ	TRY1_CANFA		TRY1_RAT	TRY3_SALSA	TRY4_RAT		KLK7_RAT	KLK PIG	KLK6 MOUSE	TRYA_RAT
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TRYB_RAT KLK8_RAT	TRY2_SALSA KLK2_CAVPO	KLK3_MOUSE TRY1_SALSA	ESTA_CANFA	KLKR PRANA	KLKC RAT	TRY2 HUMAN	TRYX GADMO	KLK4_HUMAN
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ALIGNMENTS

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EXEQUENCE FROM N.A. (ISOFORM 2).

Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,

Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,

Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,

A Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,

Andreise T., Trankheim M., Attix C., Amico-Keller G., Coeffield J.,

Andreise T., Trankheim M., Attix C., Amico-Keller G., Coeffield J.,

Andreise T., Trankheim M., Attix C., Amico-Keller G., Coeffield J.,

Andreise T., Trankheim M., Attix C., Amico-Keller G., Coeffield J.,

Andreise T., Trankheim M., Attix C., Amico-Keller G., Coeffield J.,

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Andreise T., Trankheim M., Attix C., Amico-Keller G., Coeffield J.,

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MEDLINE=20118156; PubMed=10652563;
Yousef G.M., Luo L.-Y., Diamandis E.P.;
"Identification of novel human kallikrein-like genes on chromosome 19q13.3-q13.4.";
Anticancer Res. 19:2843-2852(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
Yousef G.M., Magklara A., Scorilas A., Diamandis E.P.;
"Cloning of new alternatively spliced forms of the kallikrein-like gene 5 (KLK-L5).";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                       Q9UKR0; Q9UKR1;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Kallikrein 12 precursor (EC 3.4.21.-) (Kallikrein-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=20510030; PubMed=11054574;
Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig
Moss P., Paeper B., Wang K.;
"Sequencing and expression analysis of the serine protease gen
cluster located in chromosome 19q13 region.";
Gene 257:119-130(2000).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
NCBI_TaxID=9606;
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SIMILARITY: Belongs to peptidase family
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KLK12 OR
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This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wamodified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
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EMBL; AF135025; AAAC33365.1; -...
EMBL; AF243527; AAG33365.1; -...
EMBL; AC011473; AAG33365.1; -...
EMBL; AC011473; AAG23258.1; -...

RSP; P00763; IDPO.

RGenew, HGNC: 6360; KLK12.

MIM; 605539; -...

GO; GO: 0006508; F: Berine-type endopeptidase activity; NAS.
GO; GO: 0006508; P: Proteolysis and peptidolysis; NAS.
GO; GO: 0006508; P: Proteolysis and peptidolysis; NAS.
InterPro; IPR001254; Peptidase_S1.

RINTERPO: IPR001314; Peptidase_S1A.
PRINTS; PR00722; CHYMOTRYPSIN.
RAMART; SM00020; Tryp SPC; 1...
PROSITE; PS00134; TRYPSIN DOM; 1...
PROSITE; PS00134; TRYPSIN SER; 1...
PROSITE; PS00135; TRYPSIN SER; 1...
PROFECTION SER; 1...
PROSITE; PS00135; TRYPSIN SER; 1...
PROFECTION SER; 1.
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Mismatches 0;
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SEQUENCE OF 1-164 FROM N.A. (ISOFORM 1).

SEQUENCE OF 1-164 FROM N.A. (ISOFORM 1).

Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,

Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,

Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,

Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Garnes J.,

A Danganan L., Erler A., Christensen M., Terry A., Brower A., Garnes J.,

A Andreise T., Trankheim M., Attix C., Amico-Keller G., Coefield J.,

A Danganan L., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,

A Arellano A.S., Carrano A.V.;

A Arellano A.S., Carrano A.V.;

Sequence analysis of chromosome 19q13.4.";

Sequence analysis of chromosome 19q13.4.";

Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: Suggested to be involved in kindling epileptogenesis and hippocampal plasticity.

-I- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.

-I- SUBCELULAR LOCATION: Secreted.

-I- ALTERNATIVE PRODUCTS:
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Gan L., Gelinas R., Gown A.M., Moss P., Smith R., Wang K.;
"Molecular cloning and characterization of a novel serine protease,
ovasin, a potential molecular marker for ovarian carcinomas.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

TISSUE=Brain;

MEDLINE=99203457; PubMed=10102990;

Mitsui S., Tsuruoka N., Yamashiro K., Nakazato H., Yamaguchi N.;

"A novel form of human neuropsin, a brain-related serine protease, generated by alternative splicing and is expressed preferentially human adult brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=20510030; PubMed=11054574;
Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.
Moss P., Paeper B., Wang K.;
"Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region.";
Gene 257:119-130(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shigemasa K., Parmley T.H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Cvary;

MEDLINE=99413504; PubMed=10485494;

MEDLINE=99413504; PubMed=10485494;

Underwood L.J., Tanimoto H., Wang Y., Shigemasa K., Parmley T.F.O'Brien T.J.;

"Cloning of tumor-associated differentially expressed gene-14, serine protease overexpressed by ovarian carcinoma.";

Cancer Res. 59:4435-4439(1999).
                                                                                                                                                                                                                         Craniata; Vertebrata; Eutelo Catarrhini; Hominidae; Homo
                  KLK8 HUMAN STANDARD; PRT; 260 AA. 060259; Q9HCB3; Q9UIL9; Q9UQ47; 15-JUL-1999 (Rel. 38, Created) 15-JUL-1999 (Rel. 38, Last sequence update) 15-JUL-1999 (Rel. 43, Last annotation update) Neuropsin precursor (EC 3.4.21.-) (NP) (Kallikrein protease TADG-14) (Tumor-associated differentially
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Name=1;
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0;
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE=Hippocampus;
MEDLINE=98372070; PubMed=9714609;
Yoshida S., Taniguchi M., Hirata A.,
"Sequence analysis and expression of Gene 213:9-16(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eur. J. Biochem. 260:627-634(1999)
                                                                                                                                                                                KLK8 OR PRSS19 OR TADG14 OR NRPN
                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI TaxID=9606;
                                                                                                                                                                                                      (Human)
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KLK8_HUMAN
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Q61955;
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             Name=2;
IsoId=060259-2; Sequence=VSP 005401;
TISSUE SPECIFICITY: Isoform 1 is predominantly expressed pancreas while isoform 2 is expressed in adult brain an hippocampus. Both forms are also found in fetal brain a placenta. Not detected in kidney, spleen, liver and lun SIMILARITY: Belongs to peptidase family SI. Kallikrein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the El European Bioinformatics Institute. There are no restiby non-profit institutions as long as its content
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GO; GO: 0007399; P: neurogenesis; TAS.
InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_HIS; 1.
Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal Alternative splicing.
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13; AAG23254.1;
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AB012761;
AB010780;
AB008390;
AB008927;
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AF095742;
AF243527;
AC011473;
Q61955;
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MIM; 605644;
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STRAIN=Czech II; TISSUE=Mammary gland;

A Strausberg R.L., Pebbed=12477932;

A Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,

A Alaschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusha K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., William D.K., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

A Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Marra M.A.,

Roderation and initial analysis of more than 15,000 full-length

Rodriguez A.C., All M. A.C., Sheyer C., M., Marra M.A.,

Roderation and initial analysis of more than 15,000 full-length

Rodriguez A.C., A. Rodriguez C., M., Marra M.A.,

Rodriguez C.D., A. Rodriguez C., M., Marra M.A.,

Rodriguez C.D., Rodriguez C., M., Marra M.A.,

Rodriguez C.D., Rodriguez C., Grimman and initial analysis of more than 15,000 full-length
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STRAIN=BALB/c; TISSUE=Brain;
MEDLINE=98225202; PubMed=9556608;
Shimizu C., Yoshida S., Shibata M., Kato K., Momota Y., Matsumoto K., Shiosaka T., Midorikawa R., Kamachi T., Kawabe A., Shiosaka S.;
"Characterization of recombinant and brain neuropsin, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=BALB/c; TISSUE=Hippocampus;
MEDLINE=95348817; PubMed=7623137;
Chen Z.-L., Yoshida S., Kato K., Momota Y., Suzuki J., Tanaka T.,
Ito J., Nishino H., Aimoto S., Kiyama H., Shiosaka S.;
"Expression and activity-dependent changes of a novel limbic-serine protease gene in the hippocampus.";
J. Neurosci. 15:5088-5097(1995).
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Sciurognathi; Muridae; Mus
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"Cloning and assignment of mouse neuropsin gene, Prss19 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
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15-JUL-1999 (Rel. 38, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Neuropsin precursor (EC 3.4.21.-) (NP) (Kallikrein
KLK8 OR PRSS19 OR NRPN.
Mus musculus (Mouse).
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Mammalia; Butheria; Rodentia;
NCBI_TaxID=10090;
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                               TISSUE=Hippocampus;

MEDLINE=99134351; PubMed=9933620;

Kishi T., Kato M., Shimizu T., Kato K., Matsumoto K., Yoshida & Shiosaka S., Hakoshima T.;

"Crystal structure of neuropsin, a hippocampal protease involved in Kindling epileptogenesis.";

J. Biol. Chem. 274:4220-4224(1999).

J. Biol. Chem. 274:4220-4224(1999).

-!- FUNCTION: Suggested to be involved in kindling epileptogenesis.";

-!- FUNCTION: Suggested to be involved in kindling epileptogenesis.";

-!- FUNCTION: Suggested to be involved in kindling epileptogenesis.";

-!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.

-!- CATALYTIC ACTIVITY: Expressed specifically in the limbic symbolity.

-!- SUBCELLULAR LOCATION: Secreted.

-!- SUBCELLULAR LOCATION: Secreted.

-!- TISSUE SPECIFICITY: Expressed specifically in the limbic symbols brain and is localized at highest concentration in proposampal CAl-3 subfields.

-!- MASS SPECTROMETRY: MW=26229; METHOD=MALDI; RANGE=29-260.

-!- MASS SPECTROMETRY: MW=26229; METHOD=MALDI; RANGE=33-260.

-!- SUMILARITY: Belongs to peptidase family S1. Kallikrein subsection and is localized at highest concentration in proposampal CAL-3 subfields.
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ity
                                                      Yoshida
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CHARGE RELAY
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EMBL; AB032202; BAA92435.1; -.
EMBL; BC055895; AAH55895.1; -.
PIR; I56559; I56559.
PDB; INPM; 23-MAR-99.
MEROPS; S01.244; -.
MGD; MGI:892018; Klk8.
InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_ER; 1.
Hydrolase; Serine protease; Glycoprotei
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                           ANGSTROMS)
plasticity-related serine protease."
J. Biol. Chem. 273:11189-11196(1998)
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O88780;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neuropsin precursor (EC 3.4.21.-) (NP) (Kallikrein B) (Brain serine protease 1).

KLK8 OR PRSS19 OR NRPN OR BSP1.

Rattus norvegicus (Rat).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus NCBI_TaxID=10116;
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Pred. No. 5.1e-44;
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Best Local Similarity 49.0%;
Matches 121; Conservative
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      SEQUENCE FROM N.A.
STRAIN=Fischer; TISSUE=Brain;
MEDLINE=98389725; PubMed=9722524;
MEDLINE=98389725; PubMed=9722524;
Davies B.J., Pickard B.S., Steel M., Morris R.G.M., Lingerine proteases in rodent hippocampus.";
J. Biol. Chem. 273:23004-23011(1998).
-!- FUNCTION: Suggested to be involved in kindling ep:
hippocampal plasticity. Has a strong proteolytic and the protection (By similarity).
-!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, in CATALYTIC ACTIVITY: Restricted (By similarity).
-!- SUBCELLULAR LOCATION: Secreted (By similarity).
-!- TISSUE SPECIFICITY: Restricted to hippocampus.
-!- SIMILARITY: Belongs to peptidase family S1. Kalli
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InterPro; IPR001314; Peptidase S1A.
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PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPc; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
Hydrolase; Serine protease; Glycop
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MEROPS; S01.244; -.
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MEDLINE=22388257; PubMed=12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 1).

Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,

Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,

Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Garnes

Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu

Andreise T., Trankheim M., Attix C., Amico-Keller G., Coefield J.,

Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,

Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,

Olsen A.S., Carrano A.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

TISSUE=Hippocampus, and Prostate;

MEDLINE=20329229; PubMed=10872828;

Mitsui S., Yamada T., Okui A., Kominami K., Uemura H., Yamaguchi "A novel isoform of a kallikrein-like protease, TLSP/hippostasin, (PRSS20), is expressed in the human brain and prostate.";

Biochem. Biophys. Res. Commun. 272:205-211(2000).
                                                                                                                                                                                                                                           (Trypsin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Hippocampus;
MEDLINE=98438738; PubMed=9765601;
Yoshida S., Taniguchi M., Suemoto T., Oka T., He X.P., Shiosaka !
"CDNA cloning and expression of a novel serine protease, TLSP.";
"cDNA cloning and expression of a novel serine protease, TLSP.";
Biochim. Biophys. Acta 1399:225-228(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi
Catarrhini; Hominidae; Homo.
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MEDLINE=20130117; PubMed=10662548;
Yousef G.M., Scorilas A., Diamandis E.P.;
"Genomic organization, mapping, tissue expression, and hor regulation of trypsin-like serine protease (TLSP PRSS20), member of the human kallikrein gene family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Sequence analysis of chromosome 19q13.4."; Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                           let annotation update)
(EC 3.4.21.-) (Hippostasin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20510030; PubMed=11054574;
Gan L., Lee I., Smith R., Argonza-Barrett R., Lei
Moss P., Paeper B., Wang K.;
"Sequencing and expression analysis of the serine
cluster located in chromosome 19q13 region.";
Gene 257:119-130(2000).
                 KLKB HUMMAN CONTINE CO
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Mammalia, Eutheria, Primates;
STANDARD;
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KLK11 OR PRSS20 OR
Homo sapiens (Humar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIM; 6044344; -. 6044344; -. 60008236; F:serine-type peptidase activity; TAS. InterPro; IPR00103; Cy8 Ser trypsin.

InterPro; IPR001254; Peptidase_S1.

InterPro; IPR001314; Peptidase_S1.

InterPro; IPR001314; Peptidase_S1A.

PR00189; trypsin; 1.

PR01TE; PS00209; Trypsin, 1.

PROSITE; PS0240; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN HIS; 1.

PROSITE; PS00135; TRYPSIN JOM; 1.

PROSITE; PS00136; TRYPSIN JOM; 2.

PROSITE JOM; 2.

PROSITE; PS00136; TRYPSIN JOM; 2.

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PROSI
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TISSUE SPECIFICITY: Expressed in brain, skin and
1 is expressed preferentially in brain; isoform 2
SIMILARITY: Belongs to peptidase family S1. Kalli
                                                                                                                                                                                                                                                                                                                                                                  IsoId=Q9UBX7-1; Sequence=Displayed;
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EMBL; AB013730; BAA88713.1; -.
EMBL; AB041036; BAA96797.1; -.
EMBL; AF164623; AAD47815.1; -.
EMBL; AF243527; AAG33364.1; -.
EMBL; AC011473; AAG23257.1; -.
EMBL; BC022068; AAH22068.1; -.
HSSP; P00763; 1DPO.
MEROPS; S01.257; -.
Genew; HGNC:6359; KLK11.
MIM; 604434; -.
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                                                                                                                                                                        CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGA--STSHEHDLRLLRLRLPVRV
                                                                                                                                                                                                                                                                                           TSNMVCAG-GVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVD
                                                                                                                LSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH
                                                                                                                                                                                                                                   TSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI
                                                                                                                                                                                                                                                    4 LOLILLALATGLVGGET-RIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAH
                                                                                                                                                                                          Gaps
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Dihanich M.E., Spiess M.;
"A novel serine proteinase-like sequence from human brain.";
Biochim. Biophys. Acta 1218:225-228(1994).
-!- FUNCTION: Protease whose physiological substrate is not
-!- SUBCELLULAR LOCATION: Secreted (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=11010966;
Yousef G.M., Scorilas A., Jung K., Ashworth L.K., Diamandis
Yousef G.M., Scorilas A., Jung K., Ashworth L.K., Diamandis
"Molecular cloning of the human kallikrein 15 gene (KLK15).
regulation in prostate cancer.";
regulation in prostate cancer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the serine protease region.";
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                                                        Length
                                                                                    Indels
                           CRC64;
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        KLKF
        HUMAN
        STANDARD;
        PRT;
        256 AA.

        Q9H2R5;
        Q15358;
        Q9H2R3;
        Q9H2R4;
        Q9H2R6;
        Q9HBG9;

        16-OCT-2001
        (Rel. 40, Last sequence update)

        28-FEB-2003
        (Rel. 41, Last annotation update)

        Kallikrein
        15 precursor
        (EC 3.4.21.-)
        (ACO protease)

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=4;
                                                          j;
                                                                                    89;
(in isoform 2).
/FTId=VSP 005402.
192D910BBCDC7A56
                                                        45.0%; Score 618.5; DB 48.2%; Pred. No. 1e-43;
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IsoId=Q9H2R5-2; Sequence=VSP_005405;
                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=Q9H2R5-1; Sequence=Displayed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=20510030; PubMed=11054574;
Gan L., Lee I., Smith R., Argonza-Barri
Moss P., Paeper B., Wang K.;
"Sequencing and expression analysis of
cluster located in chromosome 19q13 re
Gene 257:119-130(2000).
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                           27466 MW;
                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                        WIRMIMRNN
                           250 AA;
                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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Matches 120
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                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                   and in the
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                          gland. Also
                                                       subfamily.
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Y SIMILARITY).
(POTENTIAL).
(POTENTIAL).
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HSSP; P00763; 1DPO.

GO; GO:0005576; C:extracellular; NAS.

GO; GO:0004252; F:serine-type endopeptidase activity; NAS.

GO; GO:0006508; P:proteolysis and peptidolysis; NAS.

GO; GO:0006508; P:proteolysis and peptidolysis; NAS.

InterPro; IPR001254; Peptidase_S1.

InterPro; IPR001314; Peptidase_S1.

R InterPro; IPR001314; Peptidase_S1.

R PROSITE; PS00134; TRYPSIN DOM; 1.

R PROSITE; PS00134; TRYPSIN JOM; 1.

R PROSITE; PS00135; TRYPSIN JES; FALSE NEG.

Hydrolase; Serine protease; Glycoprotein; Signal; Zymogen;

Alternative splicing.

Alternative splicing.
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                                     glande
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173 HGVYPGRITSNMVCAGGV-PGQDACQGDSGGPLVCGGVLQGLVSWGSVG
                 IsoId=Q9H2R5-4; Sequence=VSP_005404;
TISSUE SPECIFICITY: Highest expression in the thyroid gexpressed in the prostate, salivary, and adrenal glands colon testis and kidney.
SIMILARITY: Belongs to peptidase family S1. Kallikrein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IFLLLCVLGLSQAAT--PKIFNGTECGRNSQPWQVGLFEGTSLRCGGVL
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(in isoform 4).
SP 005404.
(in isoform 2).
SP 005405.
VSP 005407
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(BY
(BY
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(in isoform 3).
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                                                                                                                                                                                                                                                                                                                                                                                CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
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SHNEPGTAGSPRSQ ->
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Mismatches
IsoId=Q9H2R5-3; Sequence=VSP_005406,
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Missing (in |
/FTId=VSP 00:
V -> G (in is
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                                                                                                                                                 AF242195; AAG09469.1; -...
AF242195; AAG09470.1; -...
AF242195; AAG09471.1; -...
AF243527; AAG09472.1; -...
X75363; CAA53145.1; ALT_SE
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ilarity 47.1%;
Conservative 32
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256 AA;
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                       23
181 DKSYPGRLTNTMVCAGAEGRGAESCEGDSGGPLVCGGILQGIVSWGDV-PCDNTTKPGVY
                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arg-|-Xaa, Lys-|-Xaa (By similarity).
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MEDLINE=95251611; PubMed=7733885;
Wang K., Gan L., Lee I., Hood L.E.;
"Isolation and characterization of the chicken trypsinogen gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     family.";
Biochem. J. 307:471-479(1995).

Biochem. J. 307:471-479(1995).

-!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys
-!- COFACTOR: Binds 1 calcium ion per subunit (By similarity)
-!- COFACTOR: Binds 1 calcium ion per subunit (By similarity)
-!- SUBCELLULAR LOCATION: Extracellular.
-!- TISSUE SPECIFICITY: High levels are seen in the pancreas
lower levels are found in the liver, spleen and thymus.
-!- SIMILARITY: Belongs to peptidase family S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CALCIUM (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
CALCIUM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILA!
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                     LACOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Trypsin II-P29 precursor (EC 3.4.21.4).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebra Archosauria; Aves; Neognathae; Galliformes; Phas Gallus.
NCBI_TaxID=9031;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U15157; AAA79914.1; -.
PIR; S55066; S55066.
HSSP; P00763; 1DPO.
MEROPS; S01.151; -.
InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1.
PRam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
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                                                                 TYICKYVDWIRMIMRNN
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TKVCHYLEWIRETMKRN
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Calcium-binding;
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MEDLINE=21250997; PubMed=11352573;
Hooper J.D., Bui L.T., Rae F.K., Harvey T.J., Myers S.A., Ashworth L.K., Clements J.A.;
"Identification and characterization of KLK14, a novel ks serine protease gene located on human chromosome 19q13.4 in prostate and skeletal muscle.";
Genomics 73:117-122(2001).
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Kallikrein 14 precursor (EC 3.4.21.-) (Kallikrein-like
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; H
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                           569.5; DB 1;
No. 1e-39;
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SEQUENCE FROM N.A.
Yousef G.M., Diamandis E.P.;
"Molecular characterization, mapping, and tiss "Molecular characterization, mapping, and tiss a hormonally regulated kallikrein-like gene.";
a hormonally regulated kallikrein-like gene.";
c..hmitted (JUN-1999) to the EMBL/GenBank/DDBJ
                                                                                           Score 569.5; Pred. No. 1e-3:39; Mismatches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                            Ashworth L.K.
                                                                                                       the human
                             MEDLINE=20545474; PubMed=10969073;
Harvey T.J., Hooper J.D., Myers S.A., Stephenson S.A., Ashworth L. Clements J.A.;
Clements J.A.;
Tissue-specific expression patterns and fine mapping of the huma kallikrein (KLK) locus on proximal 19q13.4.";
J. Biol. Chem. 275:37397-37406(2000).
-1- SUBCELLULAR LOCATION: Secreted (Probable).
-1- TISSUE SPECIFICITY: High expression in brain, bone marrow and fetal liver. Also expressed in liver, pancreas, fetal spleen, prostate and skeletal muscle.
-1- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamer.
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GO; GO:0004252; F:serine-type endopeptidase activity; NAS.
GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
InterPro; IPR001254; Peptidase_SI.
InterPro; IPR001314; Peptidase_SI.
InterPro; IPR001314; Peptidase_SI.
PERM; PR00122; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS00134; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
THYdrolase; Serine protease; Signal; Zymogen.
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EMBL; AF283669; AAK48523.1; -.
EMBL; AC011473; AAK48524.1; -.
EMBL; AC011473; AAG23260.1; -.
HSSP; P00763; 1DPO.
MEROPS; S01.029; -.
Genew; HGNC:6362; KLK14.
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Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,

Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,

Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,

Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Garnes

A Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu

A Andreise T., Trankheim M., Attix C., Amico-Keller G., Coefield J.,

A Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,

A Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,

A Olsen A.S., Carrano A.V.;

"Sequence analysis of chromosome 19q13.4.";

Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

-!- SUBCELLULAR LOCATION: Secreted (Probable).

-!- TISSUE SPECIFICITY: Skin, thymus, trachea, cerebellum and spin
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9 precursor (EC 3.4.21.-) (Kallikrein-like)
                                                                                                                                                                                                         Vertebrata; ; ; Hominidae;
                                                                                                                                                                                                                                                            MEDLINE=20118156; PubMed=10652563;
Yousef G.M., Luo L.-Y., Diamandis E.P.;
"Identification of novel human kallikrein-like genes 19q13.3-q13.4.";
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MEDLINE=20510030; PubMed=11054574;
Gan L., Lee I., Smith R., Argonza-Barra
Moss P., Paeper B., Wang K.;
"Sequencing and expression analysis of cluster located in chromosome 19q13 re
Gene 257:119-130(2000).
                                                                                                                                                                                                                                                                                                                                     MEDLINE=20247258; PubMed=10783266;
Yousef G.M., Diamandis E.P.;
"The expanded human kallikrein gene
molecular cloning of a new member, R
Genomics 65:184-194(2000).
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EMBL; AF243527; AAG33362.1
EMBL; AC011473; AAG23255.1
HSSP; P00763; 1DPO.
                                                     25
                                                                                                          STANDARD;
                                ICKYVDWIRMIMRN
                                                     LCKYRSWIEETWRD
                                                                                                                                                                                               (Human)
                                                                                                                                                                                              Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                   N.A.
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                        Anticancer Res.
                                                                                                                                                                                                                              NCBI TaxID=9606
                                                                                                                                                                                                                                                  EQUENCE FROM
                                                                                                                              16-OCT-2001
16-OCT-2001
28-FEB-2003
Kallikrein 9
                                                                                                         KLK9 HUMAN
                                234
                                                     237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cord
           179
                                                                                                                    Q9UKQ9;
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HUMAN
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KLK9
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                                                                                               XLK9
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62 AHCRKPYLWVRLGEHHLWKWEGPEQL----PRVTDFFPHPGFNKDLSAN-DHNDDIMLIR
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                                 Genew; HGNL:000.00,

Min; 605504; ...

GO; GO:0004525; F:serine-type endopeptidase activity; NAS.

GO; GO:0004525; F:serine-type endopeptidase activity; NAS.

R InterPro; IPR001314; Peptidase_S1.

R InterPro; IPR001314; Peptidase_S1.

R Pfam; PF00089; trypsin; 1.

R PRANT; PR001314; Peptidase_S1.

R PRNTNS; PR00122; CHTMOTRYPSIN.

R PRNTNS; PR00122; CHTMOTRYPSIN.

R PROSITE; PS00134; TRYPSIN_DOM; 1.

R PROSITE; PS00134; TRYPSIN_DOM; 1.

R PROSITE; PS00134; TRYPSIN_BER; 1.

R Hydrolase; Serine protease; Glycoprotein; Signal.

FT CHAIN 16 250 KALLIKREIN 9.

FT CHAIN 16 250 KALLIKREIN 9.

FT ACT_SITE 204 204 CHARGE RELAY SYSTEM (BY SIMILAR FT ACT_SITE 204 204 CHARGE RELAY SYSTEM (BY SIMILAR FT ACT_SITE 204 204 CHARGE RELAY SYSTEM (BY SIMILAR FT DISULFID 143 210 BY SIMILARITY.

FT DISULFID 143 210 BY SIMILARITY.

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FT CARBOHYD 166 166 N-LINKED (GLCNAC. ..) (POTENT FT CARBOHYD 131 N-LINKED (GLCNAC. ..) (POTENT FT CARBOHYD 166 166 N-LINKED (GLCNAC. ..) (POTENT FT CARBOHYD 11 N-LINKED (GLCNAC. ..) (POTENT FT CARBOHYD 121 LINKED (GLCNAC. ..) (POTENT FT CAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vertebrata; 1
l; Hominidae;
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Pred. No. 1.3e-39;
32; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVT---
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Catarrhini;
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Bukaryota; Metazoa; Chordata;
Mammalia; Butheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               247
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ilarity 46.7%;
Conservative 3:
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HGNC:6370; KLK9
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119; Conser
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Biochem. J
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HSSP;
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                        ikrein-like
                                                                                                            D W
                                                                                                                                                                                                                                                                                                          subfamily
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                                                                                 Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V., Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S., Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Garnes Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu Andreise T., Trankheim M., Attix C., Amico-Keller G., Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B., Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.S., Carrano A.V.;
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cancer tie
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GO:0005576; C:extracellular; NAS.
GO:0004252; F:serine-type endopeptidase activity; NAS.
GO:0006508; P:proteolysis and peptidolysis; NAS.
erPro; IPR009003; Cys Ser trypsin.
erPro; IPR001254; Peptidase S1.
erPro; IPR001314; Peptidase S1A.
                                                                                                                                                                                                                                                                                                        S1. Kallikrein
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                                                                                                                                                                                                                                          Ansorge W., Wirkner U., Mewes H.-W., Gassenhuber J., Wier
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Secreted (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YPKTLQCAN -> GMHPHRWPEAP
BA8A9E8DCFB5D542 CRC64;
                                                                                                                                                                                 "Sequence analysis of chromosome 19q13.4.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Secreted (Probable). TISSUE SPECIFICITY: Expressed in prostate, breast,
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SYSTEM
MEDLINE=20229789; PubMed=10766816;
Yousef G.M., Chang A., Diamandis E.P.;
"Identification and characterization of KLK-L4, sense that appears to be down-regulated in breast J. Biol. Chem. 275:11891-11898 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein; Signal POTENTIAL.
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BY SIMILARITY.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                           salivary gland.
SIMILARITY: Belongs to peptidase family
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BY SIMILARITY.
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EMBL; AC011473; AAG23259.1; -.
EMBL; AL050220; CAB43320.1; ALT_INIT
HSSP; P00763; 1DPO.
MEROPS; S01.306; -.
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CHARGE
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PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPc; 1.
PROSITE; PS50240; TRYPSIN DOM; 1
PROSITE; PS00134; TRYPSIN HIS; 1
PROSITE; PS00135; TRYPSIN SER; 1
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203 B
239 B
30 N
225 N
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30570 MW;
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                                                                                                                                                                                                                      OF 1-180 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; S01.306; -.
HGNC:6361; KLK13.
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277
76
124
218
178
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116; Conser
                                                                       EQUENCE FROM N.A.
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124
218
611
157
1157
214
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225
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SIGNAL
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SEQUENCE
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ACT_SITE
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Best Local
Matches 11
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Gaps

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Conservative

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                                                                                                                                                                                                196
                                                                                                                                                                             ITSNMVCAGGVP-GQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYV
                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
GTECGRNSOPWOVGLFEGTSLRCGGVLIDHRWVLTAAH
                                                                              CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGAST--SHEHDLRLLRLRLPVRV
                                                                                                                                                         TSSVQPLPLP-NDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGR
                                                                                                                                                                                                                                                           : Arg-|-Xaa, Lys-|-Xaa
(By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             while
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE=Pancreas;
MEDLINE=95251611; PubMed=7733885;
Wang K., Gan L., Lee I., Hood L.E.;
"Isolation and characterization of the chicken trypsinogen gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; FULLO, ...

MEROPS; S01.258; ...

InterPro; IPR009003; Cyg Ser trypsin.

InterPro; IPR001254; Peptidase S1.

InterPro; IPR001254; Peptidase S1A.

RINTERPO; IPR001314; Peptidase S1A.

R PRINTS; PR00722; CHYMOTRYPSIN.

R SMART; SM00020; Tryp SPc; 1.

R PROSITE; PS50240; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN HIS; 1.

PROSITE; PS00135; TRYPSIN HIS; 1.

PROSITE; PS00135; TRYPSIN SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pancreas thymus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. J. 307:471-479(1995).

-1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-1-COFACTOR: Binds 1 calcium ion per subunit (By si-1-SUBCELLULAR LOCATION: Extracellular.
-1- TISSUE SPECIFICITY: High levels are seen in the lower levels are found in the liver, spleen and -1-SIMILARITY: Belongs to peptidase family S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Trypsin I-P38 precursor (EC 3.4.21.4).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Verte
                                                                                                                                                                                                                                                                                                                                                                                                                                                        248 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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PIR; S55067; S55067.
HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                  246
                                                                                                                                                                                                                                                                                                                  DWIRMIMR
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KLK5 HUMAN STANDARD
Q9Y337; Q9HBG8;
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16-OCT-2001 (Rel. 40, I
15-MAR-2004 (Rel. 43, I
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01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Trypsin I-P1 precursor (EC 3.4.21.4).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; P
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                                                                                                                  QUIRED FOR SPECIFICITY 78B79DD6FE15F0CE CRC64;
                                                                                                                                                       86;
                                                                                                                                         Score 566; DB 1
Pred. No. 2e-39;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Pancreas;
MEDLINE=95251611; PubMed=7733885;
Wang K., Gan L., Lee I., Hood L.E.;
"Isolation and characterization of
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ase; Digestion; Pancreas; 2
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Pred. No. 2.4e-39;
L; Mismatches 85;
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EMBL; U15155; AAA79>.

PIR; S55067; S55067.

HSSP; P00763; 1DPO.

MEROPS; S01.151; -.

( InterPro; IPR0019003; Cys Ser trypsin. InterPro; IPR001314; Peptidase S1.

R InterPro; IPR001314; Peptidase S1.

R PRINTS; PR00722; CHYMOTRYPSIN.

DR SMART; SM00020; Tryp SPC; 1.

DR SMART; PS50240; TRYPSIN.

DR PROSITE; PS50240; TRYPSIN.

DR PROSITE; PS50134; TRYPSIN DOM; 1.

DR PROSITE; PS00135; TRYPSIN DOM; 1.

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MEDLINE=22388257; PubMed=12477932;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length

Proc. Natl. Acad Sci. U.S.A. 99:16899-16903(2002).

"Thuman and mouse cDNA sequences.";

Proc. Natl. Acad Sci. U.S.A. 99:1689016903(2002).

"Thuman and mouse cDNA sequences.";

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fullahy S.J.,
ratne P.H.,
Hulyk S.W.,
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cheetz T.E.,
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       enzyme)
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in
                                                                                                                                                                                                                                                                            MEDLINE=20118156; PubMed=10652563;
Yousef G.M., Luo L.-Y., Diamandis E.P.;
"Identification of novel human kallikrein-like genes on chromosome
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Catarrhini; Hominidae; Homo.
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       (Stratum corneum
                                                                                                                                                                                       l expression of with possible :
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE=20510030; PubMed=11054574;

Gan L., Lee I., Smith R., Argonza-Barrett R., Lei

Moss P., Paeper B., Wang K.;

"Sequencing and expression analysis of the serine
cluster located in chromosome 19q13 region.";

Gene 257:119-130(2000).
                                                                                                                                                                                      "Purification, molecular cloning, and corneum trypsin-like serine protease w
     3.4.21.-)
(KLK-L2)
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                                                                                                                                        TISSUE=Stratum corneum;
MEDLINE=99445563; PubMed=10514489
Brattsand M., Egelrud T.;
                                                                                                                                                                                     cloning,
                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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AF135028; AAD26429.1;
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BC008036; AAH08036.1;
P00763; 1DPO.
       (EC :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION:
.....krein 5 precursor (F
(Kallikrein-like protein
KLKS OR SCTF
                                                 (Human)
                                                                                                                                                                                                                                                                  FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FROM N.A.
                                                                                                                            FROM N.A
                                                                                                                                                                                                                                                                                                                           19q13.3-q13.4.";
Anticancer Res.
                                                                                                                                                                                                                                                                                                                                          Res.
                                                                                                                                                                                                                      desquamation.";
                                                                                                                                                                                                                                   Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM TISSUE=Ovary;
                                                  sapiens
                                                                                                                                                                                                                                  Biol.
                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
EMBL;
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EMBL;
HSSP;
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237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 EHSLSQLDWTEQIRHSGF-SVTHPGYLGASTSHEHDLRLLRLRLPVRVTSSVQPLPLPND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SQAATPKIFNGTECGRNSQPWQVG-LFEGTSLRCGGVLIDHRWVLTAAHCSGSRYWVRLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITSNMVCAGGVPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhíni; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                            SIMILARITY).
SIMILARITY).
SIMILARITY).
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(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                 IndelB
                                                                                                                                                                                                                                                                                                                                                                     CRC64;
                             GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0004252; F:serine-type endopeptidase activity;
GO; GO:0008544; P:epidermal differentiation; TAS.
GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
InterPro; IPR009003; Cys Ser_trypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
                                                                                                                                                                                                             (BY
(BY
(BY
                                                                                                                                                                                              19;
83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLKA HUMAN STANDARD; PRT; 276 AA. 043240; Q9920; Q9GZW9; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) Kallikrein 10 precursor (EC 3.4.21.-) (Protease epithelial cell-specific 1). KLK10 OR PRRSL1 OR NES1. Homo sapiens (Human).
                                                                                                                                                                            Signal
                                                                                                                                                                                                                                                                                                                                                                                         ore 564.5; DB 1 red. No. 3.2e-39; Mismatches 83
                                                                                                                                                                            Glycoprotein; POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                          Score
Pred.
                                                                                                        Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease; Glycopr SIGNAL
                                                                                                                                                                                       41;
                                                                                                                                                                                                                                                                                                                                                                                         41.1%;
iilarity 45.3%;
Conservative 41
         KLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
TISSUE=Epithelium;
                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
S01.017; -
                                                                                                                                                                                                 23
2453
2453
2453
252
252
252
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252
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                     605643;
                                                                                                                                                                                                                                                                                                                                                                                                              107;
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ACT_SITE
ACT_SITE
DISULFID
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DISULFID
DISULFID
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                                                                                                                                                                                                                                                                                                               CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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Best Local
                                                                                                                                                                                                  CHAIN
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collaboration
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Scheetz
Prange C.,
Mullahy S.J.,
-tne P.H.,
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                                        gene, the expression progression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                      Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,
Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Garnes
Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu
Andreise T., Trankheim M., Attix C., Amico-Keller G., Coefield J.,
Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,
Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
Olsen A.S., Carrano A.V.;
"Sequence analysis of chromosome 19q13.4.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G.D.
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Sanchez
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MEDLINE-22388257; PubMed=12477932;

MEDLINE-22388257; PubMed=12477932;

Atrausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Mullahy S.

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                             characterization and mapping of the normal epithelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and
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L., Scheetz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lee S.W., Band V.;
tumor suppressor."
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                                                                                                                                                        J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S1. Kallikrein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the E
                                                                                                                                                                                                                                                                                                                                                 analysis of the serine protease ome 19q13 region.";
                                                                                                                                                        Squire
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prostate cancer.
SUBCELLULAR LOCATION: Secreted (Probable).
TISSUE SPECIFICITY: Expressed in breast, ovary and
DEVELOPMENTAL STAGE: Down-regulated during breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NES1
                                                                                                                                                        S.W., Beatty B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINE=20510030; PubMed=11054574;

Gan L., Lee I., Smith R., Argonza-Barrett R., Lei
Moss P., Paeper B., Wang K.;

"Sequencing and expression analysis of the serine
cluster located in chromosome 19q13 region.";

Gene 257:119-130(2000).
                                                                                                                                                                                                                                    247:580-586(1998).
MEDLINE=96320486; PubMed=8764136;
Liu X.-L., Wazer D.E., Watanabe K., Band V.;
"Identification of a novel serine protease-like
of which is down-regulated during breast cancer
Cancer Res. 56:3371-3379(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHARACTERIZATION.

MEDLINE=99025848; PubMed=9809976;

Goyal J., Smith K.M., Cowan J.M., Wazer D.E.,

"The role for NES1 serine protease as a novel

Cancer Res. 58:4782-4786(1998).

-!- FUNCTION: Has a tumor-suppressor role for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 progression.
SIMILARITY: Belongs to peptidase family
                                                                                                               SEQUENCE FROM N.A.
MEDLINE=98321170; PubMed=9647736;
Luo L.-Y., Herbrick J.A., Scherer
Diamandis E.P.;
                                                                                                                                                                                                                                 Commun.
                                                                                                                                                                                                                  gene.";
                                                                                                                                                                                                                                 Biophys. Rea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                           FROM N
                                                                                                                                                                                                              -specific
                                                                                                                                                                                             "Structural
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                              cell
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111
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SIMILARITY).
SIMILARITY).
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(IN REF. 3 AND 4)
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(BY
(BY
                                                                                                                                                                                                                                                                     MIM, b026/3; -. Gextracellular; TAS.

GO; GO:0008236; F:serine-type peptidase activity; TAILLEEPTO; IPR00103; Cys. Ser_trypsin.
InterPro; IPR001254; Peptidase_S1A.
InterPro; IPR001214; Peptidase_S1A.
Pfam, PF00189; trypsin; 1.
PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPC; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN LHS; 1.
PROSITE; PS00135; TRYPSIN SER; FALSE NEG.
Hydrolase; Serine protease; Glycoprotein; Signal; An. SIGNAL
ACT_SITE 86 86 CHARGE RELAY SYSTEM (BY ACT_SITE 86 86 CHARGE RELAY SYSTEM (BY ACT_SITE 137 137 CHARGE RELAY SYSTEM (BY DISULFID 52 162 BY SIMILARITY.
DISULFID 169 235 BY SIMILARITY.
DISULFID 201 215 BY SIMILARITY.
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DISULFID 225 250 BY SIMILARITY.
DISULFID 225 250 BY SIMILARITY.
DISULFID 225 250 BY SIMILARITY.
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DISULFID 39 39 N-LINKED (GLCNAC. . .)
CONFLICT 149 149 P --> L (IN REF. 3 AND 4 CONFLICT 149 P --> L (IN REF. 3 AND 4 CONFLICT 149 P --> L (IN REF. 3 AND 4 CONFLICT 149 P --> L (IN REF. 3 AND 4 CONFLICT 149 P --> L (IN REF. 3 AND 4 CONFLICT 149 P --> L (IN REF. 3 AND 4 CONFLICT 149 P --> L (IN REF. 3 AND 4 CONFLICT 149 P --> L (IN REF. 3 AND 4 CONFLICT 149 P --> L (IN REF. 3 AND 4 CONFLICT 149 P --> L (IN REF. 3 AND 4 CONFLICT 149 P --> L (IN REF. 3 AND 4 CONFLICT 149 P --> L (IN REF. 3 AND 4 CONFLICT 149 P --> L (IN REF. 3 AND 4 CONFLICT 149 P --> L (IN REF. 3 AND 4 CONFLICT 149 P --> L (IN REF. 3 AND 4 CONFLICT 149 P --> L (IN REF. 3 AND 4 CONFLICT 149 P --> L (IN REF. 3 AND 4 CONFLICT 149 P --> L (IN REF. 3 AND 4 CONFLICT 149 P --> L (IN REF. 3 AND 4 CONFLICT 149 P --> L (IN REF. 3 AND 4 CONFLICT 149 P --> L (IN REF. 3 AND 4 CONFLICT 149 P --> L (IN REF. 3 AND 4 CONFLICT 149 P --> L (IN REF. 3 AND 4 CONFLICT 149 P --> L (IN REF. 3 AND 4 CONFLICT 149 P --> L (IN REF. 3 AND 4 CONFLICT 149 P --> L (IN REF. 3 AND 4 CONFLICT 149 P --> L (IN REF. 3 AND 4 CONFLICT 149 P --> L (IN REF. 3 AND 4 CONFLICT 149 P --> L (IN REF. 3 AND 4 CONFLICT 149 P --> L (IN REF. 3 AND 4 CONFLICT 149 P --> L (IN REF. 3 AND 4 CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 564; DB 1; I
Pred. No. 3.3e-39;
; Mismatches 92;
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There
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30138 MW;
                                                                                                       EMBL; AF024605; AAB81602.1;
EMBL; AF055481; AAC14266.1;
EMBL; AF243527; AAG33363.1;
EMBL; AC011473; AAG23256.1;
EMBL; BC002710; AAH02710.1;
HSSP; P00763; 1DPO.
MEROPS; S01.246; -.
Genew; HGNC:6358; KLK10.
MIM; 602673; -.
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TQICKYMSWINKVIRSN
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ity).
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Trypsin precursor (EC 3.4.21.4).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                                                                                                              Wang K., Lytle L., Gan L., Hood L.E.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, :-!- COFACTOR: Binds 1 calcium ion per subunit (By similari--!- SUBCELLULAR LOCATION: Extracellular.
-!- SUBCELLULAR LOCATION: Extracellular.
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InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
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PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease; Digest: Signal; Multigene family.
Signal; Multigene family.
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CHAIN 22 244 TRYPS
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Search completed: June 15, 2004, 16:15:37 Job time: 18 secs

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version - 2004
GenCore (c) 1993
        Copyright
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sw model using search, - protein OM protein

2004, 16:13:26 June 15, Run on:

updates/sec ; Search time 20 Seconds
 (without alignments)
 1192.775 Million cell

US-10-006-856A-194 1374 Title: Perfect

1 MGLSIFLLLCVLGLSQAATP.. score: Sequence:

.....GVYTYICKYVDWIRM

248

IMENIN

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

283366 of hits satisfying chosen parameters: Total number

length: 0 length: 2000000000 seq seq Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Listing

78:* PIR Database

pirl: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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               C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000
C; Accession: 156559
R; Chen, Z.L.; Yoshida, S.; Kato, K.; Momota, Y.; Suzuki, J.; Tanaka, T.; Itc
J. Neurosci. 15, 5088-5097, 1995
A; Title: Expression and activity-dependent changes of a novel limbic-serine
A; Reference number: 156559; MUID:95348817; PMID:7623137
A; Accession: 156559; MUID:95348817; PMID:7623137
A; Accession: 156559
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-260 <RES>
A; Cross-references: GB:D30785; NID:91648847; PIDN:BAA06451.1; PID:91020091
C; Superfamily: trypsin homology
F; 33-252/Domain: trypsin homology
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28; Mismatches 93;
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S55066
trypsin (EC 3.4.21.4) II precursor, pancreatic (clone 2-P29) - chicken
N;Alternate names: trypsinogen II
C;Species: Gallus gallus (chicken)
C;Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 22-Jun-1999
C;Accession: S55066; S72347
C;Accession: S55066; S72347
R;Wang, K.; Gan, L.; Lee, I.; Hood, L.
Biochem. J. 307, 471-479, 1995 N RESULT

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Superfamily: trypsin; trypsin homology
Superfamily: trypsin; trypsin homology
Cheywords: hydrolase; pancreas; protein digestion; serine profile/Domain: signal sequence #status predicted <SIG>Cheywords: hydrolase; pancreas; protein digestion; serine profile/Domain: activation peptide #status predicted <APT>Cheyword: trypsin II #status predicted <AAT>Cheyword: trypsin homology <TRY>Cheyword: trypsin homology <TRY>Chewword: trypsin homology <TRY>C
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                                                 PMID: 7733885
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A; Title: Isolation and characterization of the clark Reference number: S55065, MUID:95251611; PMID: A; Accession: S55066
A; Molecule type: mRNA
A; Residues: 1-248 <WAN1>
A; Residues: 1-248 <WAN1>
A; Experimental source: clone 2-P29
A; Accession: S72347
A; Molecule type: DNA
A; Residues: 1-248 <WAN2>
A; Residues: 1-248 <WAN2>
A; Cross-references: EMBL:U15157; NID:g603906; PI
A; Residues: 1-248 <WAN2>
A; Cross-references: EMBL:U15157; NID:g603906; PI
A; Experimental source: clone 2-P29
C; Superfamily: trypsin; trypsin homology
C; Keywords: hydrolase; pancreas; protein digestiff; 11-16/Domain: signal sequence #status predicted <F; 11-25/Domain: activation peptide #status predicted <F; 26-248/Product: trypsin II #status predicted <F; 26-241/Domain: trypsin homology <TRY>
F; 65, 109, 202/Active site: His, Asp, Ser #status
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LYPPAIN (EC 3.4.21.4) precursor - pig (tentative sequence)

Ny Contains: trypsingen
Cypecies: Sus scrofa domestica (domestic pig)
Cybate: 24.Apr.1984 #sequence revision 24.Apr.1984 #text_change 31-Mar-2000
Cybate: Sus scrofa domestica (domestic pig)
Cybate: Sus scrofa dowestica (domestic pig)
Cybate: Sus scrofa 69, 115-129, 1063
A; Charles, M.; Rovery, M.; Guidoni, A.; Desnuelle, P.
B; Charles, M.; Rovery, M.; Guidoni, A.; Desnuelle, P.
A; Reference number: A90641
A; Molecule trype: protein
A; Residues: 1-10 cCHA>
A; Residues: 1-10 cCHA>
A; Residues: 1-10 cCHA>
A; Residues: 1-10 cCHA>
A; Residues: 1-10 cCHA>
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A; Residues: 1-10 cCHA>
A; Residues: 1-10 cCHA>
A; Residues: 1-10 cCHA>
A; Residues: 1-21 cHER>
A; Residues: 9-211 cHER>
A; Residues: protein
A; Residues: product: trypsin pertide #status experimental cAPT>
F; 1-31/Product: trypsin pertide #status experimental cAPT>
F; 1-31/Product: trypsin #status experimental cAPT>
F; 1-31/Product: trypsin #status experimental cAPT>
F; 1-34/Domain: activation peptide #status experimental cAPT>
F; 1-34/Domain: trypsin homology cTRY, 181-205/Disulfide bonds: #status predicted
F; 1-148, 92, 185/Active site: His, Asp, Ser #status predicted
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               PID:9603903
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A;Cross-references: GB:U15155; NID:g603902; PIDN:AAA79912.1; PID:gA;Experimental source: clone Pl
R;Wang, K.
submitted to the EMBL Data Library, September 1994
A;Reference number: S71155
A;Accession: S71155
A;Accession: S71155
A;Accession: S71155
A;Residues: 1-102,'A',104-248 <WANS>
A;Residues: 1-102,'A',104-248 <WANS>
A;Residues: 1-102,'A',104-248 <WANS>
A;Residues: 1-102,'A',104-248 <WANS>
C;Superfemily: trypsin; trypsin homology
C;Reywords: hydrolase; pancreas; protein digestion; serine protein
C;Reywords: hydrolase; pancreas; protein digestion; serine protein
F;1-15/Domain: signal sequence #status predicted <APT>
F;26-248/Product: trypsin I #status predicted <APT>
F;26-241/Domain: trypsin homology <TRX>
F;65,109,202/Active site: His, Asp, Ser #status predicted
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88;
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C; Species: Mus musculus (house mouse)
C; Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 22-Jun-1999;
C; Accession: B2528
R; Stevenson, B.J.; Hagenbuechle, O.; Wellauer, P.K.
Nucleic Acids Res. 14, 8307-8330, 1986
A; Title: Sequence organisation and transcriptional regulation of the mouse A; Reference number: A93646; MUID:87066713; PMID:3641189
A; Accession: B2528
A; Molecule type: mRNA
A; Residues: 1-246 <STE>
A; Cross-references: GB:X04574; NID:954918; PIDN:CAA28243.1; PID:954919
C; Superfamily: trypsin; trypsin homology
C; Superfamily: trypsin; bydroluse; predicted <SIG>C; Superfamils: signal sequence #status predicted <MIS-23/Domain: trypsin homology <TRY>
F; 24-246/Product: trypsin #status predicted <MAT>
F; 24-246/Product: trypsin homology <TRY>
F; 24-239/Domain: trypsin homology <TRY>
F; 24-246/Product: trypsin homology <TRY>
F; 30-160,48-64,132-233,139-206,171-185/Disulfide bonds: #status predicted
F; 63,107,200/Active site: His, Asp, Ser #status predicted
F; 75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HGVYPGRITSNMVCAGGVPG--QDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
                serine proteinase SCCE precursor - human
N; Alternate names: stratum corneum chymotryptic enzyme
C; Species: Homo sapiens (man)
C; Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 2;
C; Accession: A53968
R; Hansson, L.; Stroemqvist, M.; Baeckman, A.; Wallbrandt, P.; Carl
J. Biol. Chem. 269, 19420-19426, 1994
A; Title: Cloning, expression, and characterization of stratum corn
A; Reference number: A53968; MUID:94308225; PMID:8034709
A; Accession: A53968
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-253 < HAN>
A; Cross-references: GB:L33404; NID:g521214; PIDN:AAC37551.1; PID:(C; Genetics:
A; Gene: GDB:PRSS6; SCCE
A; Genetics: A; Gub:377730
A; Map position: 7q35-7q35
C; Superfamily: trypsin homology < TRY>
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Pred. No. 6.3e-38
15; Mismatches 8:
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Pred. No. 4.5e-38;
7; Mismatches 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            trypsin (EC 3.4.21.4) precursor, pancreatic - African clawed frog C; Species: Xenopus laevis (African clawed frog)
C; Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 04-6
C; Accession: A35871; S1217
R; Shi, Y.B.; Brown, D.D.
Genes Dev. 4, 1107-1113, 1990
A; Title: Developmental and thyroid hormone-dependent regulation of p A; Reference number: A35871; MUID:91007255; PMID:2210372
A; Accession: A35871; MUID:91007255; PMID:2210372
A; Actus: preliminary
A; Molecule type: mRNA
A; Residues: 1-243 <SHI>
A; Cross-references: EMBL:X53458; NID:965162; PIDN:CAA37538.1; PID:9655
C; Superfamily: trypsin; trypsin homology
C; Keywords: hydrolase; protein digestion; serine proteinase
F; 1-15/Domain: signal sequence #status predicted <SIG>F; 6-243/Product: trypsin homology <TRY>F; 6-243/Product: trypsin lastatus reconstruction from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the first from the f
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1.3e-38;
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C; Species: Bos primigenius taurus (cattle)
C; Species: Bos primigenius taurus (cattle)
C; Date: 02-Dec-1993 #sequence_revision 03-Aug-1995 #text_change 22-c
C; Accession: S13813
R; le Huerou, I.; Wicker, C.; Guilloteau, P.; Toullec, R.; Puigserve; Bur. J. Biochem. 193, 767-773, 1990
A; Title: Isolation and nucleotide sequence of cDNA clone for bovine A; Reference number: S13813; MUID:91065383; PMID:1701147
A; Accession: S13813
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-247 < HUE>
A; Cross-references: EMBL:X54703; NID:9829; PIDN:CAA38513.1; PID:98365; Superfamily: trypsin homology
C; Superfamily: trypsin; trypsin digestion; serine proteinase
C; Superfamily: trypsin homology
C; Keywords: hydrolase; protein digestion; Serine proteinase
F; 24-239/Domain: trypsin homology < TRY>
F; 63,107,200/Active site: His, Asp, Ser #status predicted
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N;Alternate names: cationic trypsinogen
C;Species: Canis lupus familiaris (dog)
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 18
C;Accession: A26273
R;Pinsky, S.D.; LaForge, K.S.; Scheele, G.
Mol. Cell. Biol. 5, 2669-2676, 1985
A;Title: Differential regulation of trypsinogen mRNA translation: A;Reference number: A26273; MUID:86284628; PMID:3841794
A;Accession: A26273
A;Molecule type: mRNA
A;Residues: 1-247 <PIN>
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84;
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Best Local Similarity 45.7%; Pred. No. 1.1e-37
Matches 113; Conservative 40; Mismatches 8
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TYPESION (EC 3.4.21.4) precursor - bowine
N; Contains: trypeinogen
C; Date: 24-Apr-1894 # Sequence zevision 28-Feb-1986 #text_change 18-Jul-1997
C; Date: 24-Apr-1894 # Sequence zevision 28-Feb-1986 #text_change 18-Jul-1997
C; Date: 24-Apr-1894 # Sequence zevision 28-Feb-1986 #text_change 18-Jul-1997
C; Date: 24-Apr-1894 # Sequence zevision 28-Feb-1986 #text_change 18-Jul-1997
C; Accession: A90164; A00946; S08774*
N; Mitcle: Covalent structure of bovine trypsingen. The position of the remaining A; Accession: A90164
A; Molcoule (Type: procein
A; Reference number: A90164; MUID: 67168848; PMID: 5967094
A; Molcoule: 1-57, 70, 59-67, 70, 69-150, 7N', 152-176, 7N', 178-229 <AIK>
B; Hartley, B.S.
A; Contents: annotation; revisions
R; Mitcle: The annotation; revisions
R; Mitcle: The annotation; revisions
R; Mitcle: The sequence of dogfish trypsin
A; Reference number: A00950; MUID: 7146444; PMID: 1092332
A; Contents: annotation; revisions
R; Moccenter annotation; revisions
R; Molcoule: Trypsingen is synthetase with the actine to beta-trypsin at 1.8 angstrom
A; Rochengier: P.
A; Mitcle: The refined crystal structure of bovine beta-trypsin by releasing C; Comment: Trypsingen is synthetased with the actine to beta-trypsin by releasing C; Comment: Trypsingen is synthetased in the actine to beta-trypsin by releasing C; Comment: Trypsingen is synthetased in digestion, serrine proteinase; zymogen S; Procenter: Trypsin palao cocur after Arg-105.
C; Comment: Autocatalyric clavage may pale occur after Arg-105.
C; Comment: Autocatalyric clavage may pale occur after Arg-105.
C; Superfamily: trypsin, trypsin palao cocur after Arg-105.
C; Superfamily: trypsin palao and palao and digestion, serrine proteinase; zymogen S; Procenter: Trypsin palao-trypsin monology
C; Superfamily: trypsin palao-trypsin monology
C; Superfamily: trypsin palao-trypsin monology
C; Superfamily: trypsin palao-trypsin digestion experimental caption activation peptide #status experimental caption P; 7-131, 132-229/Product: Lyg-118-154-166,179-203/Disulfi
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 -ATPKI FNGTECGRNSQPWQVGLFEGTSLRC
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Pred. No. 7.1e-38;
); Mismatches 77;
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21 KIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAHCSGSRYWVRLGEHSLSQL

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6 KIVGGYTCGANTVPYQVSLNSGYHF-CGGSLINSQWVVSAAHCYKSGIQ

Control of the Contro

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trypsin (EC 3.4.21.4) precursor, cationic - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 22-Jun-1999
C;Accession: A27547
R;Fletcher, T.S.; Alhadeff, M.; Craik, C.S.; Largman, C.
Biochemistry 26, 3081-3086, 1987
A;Title: Isolation and characterization of a cDNA encoding rat cationic trypsi
A;Reference number: A27547; MUID:87271609; PMID:3607011
A;Reference number: A27547
A;Molecule type: mRNA
A;Residues: 1-247 <FLE>
A;Ccoss-references: GB:M16624; NID:g206498; PIDN:AAA41985.1; PID:g206499
C;Superfamily: trypsin; trypsin homology
C;Keywords: calcium binding; hydrolase; protein digestion; serine proteinase
F;25-240/Domain: trypsin homology <TRY>
F;31-161,49-65,133-234,140-207,172-186/Disulfide bonds: #status predicted
F;64,108,201/Active site: His, Asp, Ser #status predicted
F;76,78,81,86/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
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                      1 MKALIFLAFLGAAVALPLDDDDDKIVGGYTCOKNSLPYQVSLNAGYHF-CGGSLINSOWV
                                                                           #Btatus predicted
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N;Alternate names: trypsinogen I
C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_cha
C;Accession: B22657; A00948
R;Craik, C.S.; Choo, Q.L.; Swift, G.H.; Quinto, C.; MacDonal
J. Biol. Chem. 259, 14255-14264, 1984
A;Title: Structure of two related rat pancreatic trypsin gen
A;Reference number: A22657; MUID:85054880; PMID:6094547
A;Accession: B22657
A;Residues: 1-246 <CRA>
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Best Local Similarity 43.3%; Pred. No. 3.1e-37;
Matches 109; Conservative 43; Mismatches 89;
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236 VSWIQQTIAAN
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N;Alternate names: cationic trypeinogen
C;Species: Canis lupus familiaris (dog)
C;Date: 30.Sep-1987 #sequence_revision 30-Sep-1987 #text_change 18-(c;Date: 30.Sep-1987 #sequence_revision of trypsinogen mRNA translation: f
A;Reference number: A26273; MUD:86284628; PMID:3841794
A;Reference number: A26273; MUD:86284628; PMID:3841794
A;Residues: 1-246 <PIN>
A;Residues: 1-246 <PIN>
A;Residues: 1-246 <PIN>
A;Residues: aignal sequence #status predicted <SIG>C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; pancreas; protein digestion; serine proteina F;1-15/Domain: signal sequence #status predicted <ART>
F;24-246/Product: trypsin, cationic #status predicted <ART>
F;24-239/Domain: trypsin homology <TRY>
F;24-239/Domain: trypsin homology <TRY>
F;24-239/Domain: trypsin homology <TRY>
F;30-160,48-64,132-233,139-206,171-185/Disulfide bonds: #status pre
F;63,107,200/Active site: His, Asp, Ser #status predicted
F;75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status pr
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                                                                                                                                                                                                                        Length 247;
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C; Keywords: hydrolase; pancreas; protein digestion; serine prote
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-23/Domain: activation peptide #status predicted <APT>
F;24-247/Product: trypsin, anionic #status predicted <ENZ>
F;24-239/Domain: trypsin homology <TRY>
F;30-160,48-64,132-233,139-206,171-185/Disulfide bonds: #status
F;63,107,200/Active site: His, Asp, Ser #status predicted
F;75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status
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NID:g164094; PIDN:AAA30899.1;
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87;
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Pred. No. 2.9e-37
; Mismatches 8
                                                                                                                                                                                                                      39.7%; Score 546; DB 1;
larity 45.6%; Pred. No. 2.4e-37
Conservative 38; Mismatches 8
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Jutrons: 14/1; 67/2; 152/1; 197/3

Superfamily: trypsin; trypsin homology

Keywords: hydrolase; pancreas; protein digestion; serine protein signal sequence #status predicted <SIG>

Jule-23/Domain: activation peptide #status predicted <APT>

Jule-23/Domain: activation peptide #status predicted <APT>

Jule-23/Domain: trypsin lomology <TRY>

Jule-239/Domain: trypsin homology <TRY

Jule-239/Domain: trypsin homology <TRY

Jule-239/Domain: trypsin homolog
                       -references: GB:J00778; NID:g206507; PIDN:AAA98518.1; PI:
the authors translated the codon ATC for residue 6 as Lalald, R.J.; Stary, S.J.; Swift, G.H.
. Chem. 257, 9724-9732, 1982
.: Two similar but nonallelic rat pancreatic trypsinogens ence number: A00948; MUID:82265624; PMID:6896710
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S31779
trypsin (EC 3.4.21.4) III precursor - Atlantic salmon (fragmen' C; Species: Salmo salar (Atlantic salmon)
C; Date: 22-Nov-1993 #sequence_revision 03-Aug-1995 #text_changon' C; Date: 22-Nov-1993 #sequence_revision 03-Aug-1995 #text_changon' C; Accession: S66657; S31779
R; Male, R.; Lorens, J.B.; Smalas, A.O.; Torrissen, K.R.
Eur. J. Blochem. 232, 677-685, 1995
A; Title: Molecular cloning and characterization of anionic and A; Reference number: S66657; MUID: 96035908; PMID: 7556223
A; Accession: S66657
A; Molecular Cioning and characterization of anionic and A; Reference number: S66657; MUID: 96035908; PMID: 7556223
A; Accession: S66657
A; Molecular Cioning and characterization of anionic and A; Residues: 1-238 cMAL>
A; Cossereferences: EMBL: X70074; NID: 964387; PIDN: CAA49679.1; C; Superfamily: trypsin homology
C; Keywords: hydrolase; serine proteinase
F; 1-7/Domain: activation peptide #status predicted cAPT>
F; 16-238/Product: trypsin homology cTRY>
F; 16-238/Product: Hispsin homology cTRY>
F; 16-248/F; 16-25/F; 171-198/F; 16-2477/F; 16-2475/F; 16-2475/F; 16-2477/F; 16-2475/F; 16-2475/F;
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n ATC for residue 6
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;Cross-references: GB:J00778; NID:g206507; PIDN:AAA98518
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76;
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Pred. No. 4.1e-37
17; Mismatches 70
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4

Gaps

. 9

Indels

78;

238

Length

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2 DB

7e-37;

Score 540; DE Pred. No. 7e-3 37; Mismatches

39.3%;

37;

Conservative

108;

Similarity

luery Ma. at Local

Query Ma Best Loc Matches

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proteinase; zymogen
 4
 140
 199
 118
 178
 178
 237
 131
 191
 RESULT 15
S05494
trypsin (EC 3 4.21.4) IV precursor - rat
NyAlternate names: 23K protein; trypsinogen IV precursor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 22-Jun-1999
C;Accession: S05494
R;Luetcke, H.; Rausch, U.; Vasiloudes, P.; Scheele, G.A.; Kern, H.F.
Nucleic Acids Res. 17, 6736, 1989
A;Title: A fourth trypsinogen (P23) in the rat pancreas induced by CCK.
A;Reference number: S05494; MUD:89386010; PMID:2780302
A;Ression: S05494
A;Molecule trype: mRNA
A;Ressidues: 1-247 cLUE>
A;Residues: 1-247 cLUE>
A;Coss-references: EMBL:X15679; NID:g56813; PIDN:CAA33718.1; PID:g56814
C;Superfamily: trypsin; trypsin homology
C;Keywords: calcium binding; hydrolase; protein digestion; serine proteinase; F;16-23/Domain: signal sequence #status predicted <ADT>
F;24-240/Domain: trypsin homology <C;Keywords: calcium binding; hydrolase; protein digestion; serine proteinase; F;16-23/Domain: trypsin homology <C;Keywords: calcium binding; hydrolase; protein digestion; F;24-240/Domain: trypsin homology <C;Keywords: calcium binding; hydrolase; protein digestion; F;24-240/Domain: trypsin homology <C;Keywords: calcium binding; hydrolase; protein digestion; F;24-240/Domain: trypsin homology <C;Keywords: calcium dide; His, Asp, Ser #status predicted
F;64,108,201/Active site: His, Asp, Ser #status predicted
F;76,78,18,81,86/Binding site: calcium (Glu, Asn, Val, Val, Glu)
 9
 58
 22-Jun-1999
KI FNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAHCSGSRYWVRLGEHSLSQL
 VINSOVSTVSLPRSCASTDAQCLVSGWGNTVSIGGKYPALLQCLEAPVLSASSCKKSYPG
 HVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITSNMVCAGGVP-GQDACQGD
 1 MGLSIF--LLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVL
 RVTSSVOPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPG
 DWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRVTSSVQPLPLPNDCATAGTEC
 TAAHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPV
 RITSNMVCAGGVP-GQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKY
 #status predicted
 1 MKISİFFAFLGAAVALPVNDDDKİVGGYTCPKHLVPYQVSLHDGISHQCGGSLİSDQMVL
 238
 Length 247;
 SGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDWIRMIMRNN
 DB 2;
 Match
Local Similarity 43.4%; Pred. No. 2.5e-36;
Les 109; Conservative 41; Mismatches 94;
 41;
 2004,
 248
 15,
 VDWIRMIMRNN
 : ||: | ||
LSWIQETMANN
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 completed:
e : 21 sece
 Query Match
Best Local S
Matches 109
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updates/sec **JENN 248** 1 MGLSIFLLLCVLGLSQAATP......GVYTYICKYVDWIRMIN US-10-006-856A-194 1374 score: Sequence: Perfect Title:

0.5 Gapext BLOSUM62 Gapop 10.0 , Scoring table:

1586107 hits satisfying chosen parameters o£ Total number

residues

282547505

1586107 segs,

Searched:

seq length: 0 seq length: 2000000000 0B 0B Minimum Maximum

Minimum Match 0% Maximum Match 100% Listing first 45 summaries Post-processing:

Geneseq\_29Jan04:\*
geneseqp1980s:\*
geneseqp2000s:\*
geneseqp2001s:\*
geneseqp2002s:\*
geneseqp2003as:\*
geneseqp2003as:\* Geneseq 29Jan04 **مر**' .. .. .. .. .. .. .. 4 2 M 4 M 9 M 7 8 •• Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|             |      | de     |        |          | SUMMARIES |                |
|-------------|------|--------|--------|----------|-----------|----------------|
| 년 0         | COL  | ىتن    | Length | DB       | ID        | Description    |
| ;<br>;<br>; | 1374 | 100.   | 24     | F        | AAB21304  |                |
| 7           | 37   | 00     | 4      | m        | 2442      | 24428 Human    |
| m           | 37   | 100.0  | 248    | ო        | 240       | 032 Human      |
| 4           | 37   | 00.    | 4      | ĸ        | 939       | 99393 Human    |
| Ŋ           | 37   | 00     | 4      | 4        | 9         | 23994 Human    |
| 9           | 37   | 00     | 4      | 4        | 614       | 66142 Protei   |
| 7           | 37   | 00.    | 4      | ø        | 363       | 33635 Novel hu |
| 80          | 37   | 00,    | 4      | 7        | 48        | 44488 Human    |
| თ           | 37   | 00     | 4      | 7        | 351       | 33512 Novel hu |
| 10          | 37   | 00     | 4      | ۲        | 90        | 18063 Human    |
| Τī          | 37   | 00     | 4      | ~        | 070       | 7070           |
| 12          | 37   | 00.    | 4      | 7        | 978       | 9786 Human se  |
| 13          | 37   | 00     | 4      | 2        | 7023      | 70232          |
| 14          | 37   | 00.    | 4      | ,        | 35        | 38353 Human    |
| 12          | 37   | 00     | 4      | ۲        | 3930      | 3930           |
| 16          | 37   | 00.    |        | ~        | 883       | 38832 Human s  |
| 17          | 37   | 00.    | 4      | 7        | 4026      | 10263 Human se |
| 18          | 37   | 00     | 4      | 7        | 5048      | 50484          |
| 19          | 37   | 00     | 4      | 7        | 2009      | 20096 Human se |
| 20          | 37   | 00     | 4      | <b>~</b> | 0         |                |
| 21          | 37   | 00.    | 4      | _        | ADE21565  | 21565 Human    |
| 22          | 36   | ი<br>ი | 4,     | 9        |           | 29516 Human    |
| 23          | 30   | 4      | Ŋ      | സ        | AAB21303  | <del>М</del>   |
| 24          | 30   | 4      | Ŋ      | Ŋ        | 6667      | 676 Human      |
| 25          | 01   | 74.2   |        | ന        | AAB21301  | 21301 Human    |

| 26 811 59.0 162 2 AAY28642 28 630.5 45.9 260 2 AAY32852 29 630.5 45.9 260 2 AAY32220 30 630.5 45.9 260 3 AAB41322 31 630.5 45.9 260 3 AAB44300 32 630.5 45.9 260 3 AAB44300 34 630.5 45.9 260 4 AAB53087 35 630.5 45.9 260 4 AAB53087 36 630.5 45.9 260 4 AAB53087 36 630.5 45.9 260 6 ABB4852 37 630.5 45.9 260 6 ABB95458 39 630.5 45.9 260 6 ABU81067 40 630.5 45.9 260 6 ABU81067 41 630.5 45.9 260 6 ABU81067 42 630.5 45.9 260 6 ABU81067 43 630.5 45.9 260 6 ABU81067 44 630.5 45.9 260 6 ABU81067 45 630.5 45.9 260 6 ABU81067 46 630.5 45.9 260 6 ABU81067 47 630.5 45.9 260 6 ABU81067 48 630.5 45.9 260 6 ABU81067 49 630.5 45.9 260 6 ABU84932 | 28642 Human s | 2852 Human se | 741744 Human P | 322     | 2132     | 0    | 51131 Human | au1236 | 53087 Human | 2337 | 34852 Human | 81959 Human | 95458 Human | 7813 Novel | 2524 | 67 Human | 25   | 0    | 7    | Abu84932 Human sec |  |
|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------|---------------|----------------|---------|----------|------|-------------|--------|-------------|------|-------------|-------------|-------------|------------|------|----------|------|------|------|--------------------|--|
| 6 811 59.0 162<br>630.5 45.9 260<br>630.5 45.9 260                                                                                                                                                                                                                                                                                                                                                                                                                     | Y2864         | X3285         | 4174           | 0322    | 32132    | 4430 | 5113        | 31236  | 85308       | 2337 | 8485        | 8195        | 9545        | 781        | 524  | 106      | 7225 | 0570 | 9299 | 3493               |  |
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| 630.5 45.<br>630.5 45.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Ø             | ω             | Ø              | w       | v        | 9    | 9           | 9      | 9           | 9    | 9           | Θ           | 9           | 9          | Ø    | Ø        | φ    | Ø    | 9    | Θ                  |  |
| 6 6 30 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | σ.            | ω.            | ٠<br>س         | رى<br>س | <u>ر</u> | ъ.   | Ω.          | ŝ      | <u>ب</u>    | δ.   | υ.          | ъ.          | ٠<br>س      | 'n         | 'n.  | <u>ب</u> | ů.   | 5    | ហ    | 45.9               |  |
| ИИИИВВВВВВВВ 4 4 4 4 4 4 6<br>6 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | $\overline{}$ | 30.           | 30.            | 30.     | 30.      | 30.  | 30.         | 30.    | 30.         | 30.  | 30.         | 30.         | 30.         | 30.        | 30.  | 30.      | 30.  | 30.  | 30.  | 30.                |  |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 26            | 27            | 28             | 29      | 30       | 31   | 32          | 33     | 34          | 35   | 36          | 37          | 38          | 99         | 40   | 41       | 42   | 43   | 44   | <u>4</u><br>ሚ      |  |

## ALIGNMENTS

```
Human; KLK-L1; KLK-L2; KLK-L3; KLK-L4; KLK-L5; KLK-L6;
kallikrein-like protein; serine protease; cytostatic; oprostrate cancer.
 248 AA
 99US-0124260P.
99US-0127386P.
99US-0144919P.
 SINAI HOSPITAL.
 2000WO-CA000258
 AAB21304 Btandard; protein;
 entry)
 EP;
 #4
 Diamandis
 Human KLK-LS protein
 (first
 WO200053776-A2
 TNUOM (NUOM)
 11-MAR-1999;
01-APR-1999;
21-JUL-1999;
 sapiens.
 09-MAR-2000;
 14-SEP-2000.
 02-FEB-2001
 £
 AAB21304;
 Yousef
 Homo
RESULT 1
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cancer;

WPI; 2000-587440/55 N-PSDB; AAA95944.

(KLK-L) proteins for diagnosing and treating KLK-Lorders, especially cancer. disorders, New kallikrein-like protein mediated dis

Claim 12; Page 172; 184pp; English.

The present sequence is one of four alternatively spliced kallikrein-like proteins encoded by the human KLK-L4 gene. Kallikreins and kallikrein-like proteins are a subgroup of the serine protease enzyme family. They catalyse the selective cleavage of specific polypeptide precursors to release peptides with potent biological activity. Nucleic acids encoding kallikrein-like proteins KLK-L1, KLK-L2, KLK-L3, KLK-L4, KLK-L5 and KLK-L6 have been isolated. The proteins are useful in the treatment, monitoring and diagnosis of cancers, especially prostrate cancer. They can also be used to identify a substance that can associate with or mediate the biological activity of the proteins. Antibodies can be used

```
0
 120
 120
 180
 180
 240
 240
 Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation; diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy; angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic; cytostatic; gene therapy; vaccine.
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 9
 VYTYICKYVDW
 LLRLRLPVRV
 VLIDHRWYLTA
 TCHGVYPGRI
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 AHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLR
 TSSVOPLPLPNDCATAGTECHVSGWGITNHPRNPPPDLLQCLNLSIVSHA
 TSNMVCAGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGV
 protein
 ત
 CVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGG
 Length
 IndelB
kallikrein-like
 .;
0
;
 Score 1374; DB 3
Pred. No. 3.8e-98
Mismatches 0
 Human PRO1303 protein sequence SEQ ID NO:203
the
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ρχ
 248
 0;
 98WO-USO25108.

98US-0112850P.

99US-0115554P.

99US-0123957P.

99US-0131445P.

99US-0131445P.

99US-01312252.

99US-0141037P.

99US-0144758P.

99US-0144758P.

99WO-USO20594.

99WO-USO20594.

99WO-USO21090.

99WO-USO21090.

99WO-USO21090.
mediated
 Query Match
Best Local Similarity 100.0%;
Matches 248; Conservative
 99WO-US028313
 AAB24428 standard; protein;
 entry)
 248
 248
 GENENTECH INC
conditions
 (first
 MGLSIFLLL
 IRMIMRNN
 IRMIMRNN
 248 AA;
 WO200032221-A2
 01-DEC-1998;
16-DEC-1998;
12-JAN-1999;
08-MAR-1999;
12-MAY-1999;
28-APR-1999;
23-JUN-1999;
23-JUN-1999;
20-JUL-1999;
26-JUL-1999;
13-SEP-1999;
15-SEP-1999;
15-SEP-1999;
15-SEP-1999;
 Ното варіепв
 30-NOV-1999;
 08-JUN-2000.
 07-NOV-2000
 241
 Н
 61
 61
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 121
 121
 181
 181
to treat
 Sequence
 241
 AAB24428
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The present invention describes nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorder in mammals by modulating cell proliferation, angiogenesis and cardiovascularisation, and for identifying agonists and antagonists of these processes. The nucleic acids and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PRO expression such as cardiovascular, endothelial or angiogenic disorders in mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors containing them and the PRO polypeptide may be used to treat disorders associated with decreased PRO expression. AAA77510 to AAA77721 and AAB24338 to AAB24435 represent nucleotide and protein sequences used in the exemplification of the present invention
 diagnosing
 180
 240
 240
 120
 120
 180
 9
 9
 1 MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTA
 AHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRV
 61 AHCSGSRYWVRLGEHSLSQLDWTBQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRV
 TSNMVCAGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDW
 TSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI
 Gaps
 cancer;
 J;
Paoni NF;
 Nucleic acids encoding PRO polypeptides useful for preventing, dia
and treating diagnosing a cardiovascular, endothelial or angiogeni
disorders in mammals.
 ò
 248;
 diagnosis; neoplastic disease; proliferation; tumourigenesis; anticancer; detection.
 召
 Length
 Hillan F
Kuo SS,
 Indels
 Query Match
Best Local Similarity 100.0%; Score 1374; DB 3;
Best Local Similarity 100.0%; Pred. No. 3.8e-98;
Matches 248; Conservative 0; Mismatches 0;
 Gerber H,
Klein RD,
Wood WI;
 Human PRO1303 protein sequence SEQ ID NO:33
 , Ferrara N,
, Gurney AL,
Williams PM,
 Z
 72; Fig 82; 315pp; English
 248
 ·,
 standard; protein;
 entry)
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 248
 248
Ashkenazi AJ, Baker
Goddard A, Godowski
Smith V, Watanabe C
 WPI; 2000-412154/35
N-PSDB; AAA77671.
 (first
 IRMIMRNN
 IRMIMRNN
 Sequence 248 AA;
 Human; tumour; didentification;
 WO200053750-A1
 sapiens
 14-SEP-2000.
 25~JAN-2001
 AAB24032;
 61
 121
 181
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 AAB24032
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transmembrane;
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 01-SEP-1998;

01-SEP-1998;

02-SEP-1998;

02-SEP-1998;

02-SEP-1998;

03-SEP-1998;

04-SEP-1998;

05-SEP-1998;

06-SEP-1998;

10-SEP-1998;

10-SEP-1998;

10-SEP-1998;

10-SEP-1998;

10-SEP-1998;

11-SEP-1998;

11-SEP-1998;

12-SEP-1998;

12-SEP-1998;

13-SEP-1998;

14-SEP-1998;

15-SEP-1998;

17-SEP-1998;

18-SEP-1998;

17-SEP-1998;

18-SEP-1998;

18-SEP-1998;

18-SEP-1998;

18-SEP-1998;

23-SEP-1998;

23-SEP-1998;

23-SEP-1998;

24-SEP-1998;

24-SEP-1998;

24-SEP-1998;

24-SEP-1998;

24-SEP-1998;

24-SEP-1998;

25-SEP-1998;

26-SEP-1998;

27-SEP-1998;

28-SEP-1998;

28
 PRO1303
 sapiens
 09-MAR-2000
 PRO
 Human;
 Homo
The present invention describes an antibody that binds to a human protein

(I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780; PRO334;

(PRO1927; PRO3567; PRO1295; PRO1293; PRO1303; PRO444; PRO4354; PRO4397;

(PRO4407; PRO1555; PRO1096; PRO2262. (I) has anticancer activity and can be used to diagnose tumours in mammals, by detecting complex formation when the antibody is contacted with test cells.

(Increased expression of genes encoding (I) can also be detected to diagnose tumours. Agents which inhibit the activity of (I), especially the antibodies, or an antisense oligonucleotide which hybridises to genes encoding (I), can be used to inhibit tumour growth, preferably by inducing cell death. Methods from the present invention can be used to identify compounds which inhibit the biological activity of (I). AAC58019 contacting cell death. PCR primers and hybridisation probes used in examples from the present invention for human PRO sequences. AAC58103 to protein sequences given in the exemplification of the present invention
 O
 180
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 240
 inhibit
PRO
 TYICKYVDW
 TYICKYVDW
 IDHRWVLTA
 IDHRWVLTA
 LRIELPVRV
 AHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLPVRV
 CHGVYPGRI
 CHGVYPGRI
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of
 248;
 1 MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVL
 1 MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVL
 AHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRL
 TSSVOPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHAT
 TSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHAT
 TSNMVCAGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVY
 TSNMVCAGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVY
 Antibodies specific for PRO polypeptides, used to diagnose the growth of tumors in mammals, and to identify inhibitors polypeptide activity or expression.
 Watanabe CK,
 Length
 Indels
 Score 1374; DB 3;
Pred. No. 3.8e-98;
; Mismatches 0;
 ROY MA,
 Gurney AL,
 Claim 61; Fig 24; 226pp; English.
 protein; 248
 0;
 99WO-US020111.
99US-0162506P.
99WO-US028313.
99WO-US028634.
 100.08;
 100.08;
 99WO-US028551
 99WO-US005028
 (first entry)
 Query Match
Best Local Similarity 100.
 Ä
 248
 GENENTECH INC.
 248
 Goddard
 WPI; 2000-594320/56
 AAY99393 standard;
 IIIIIII
 IRMIMRNN
 Sequence 248 AA;
 N-PSDB; AACS8114
 02-DEC-1999;
 08-AUG-2000
 01-SEP-1999;
29-OCT-1999;
30-NOV-1999;
01-DEC-1999;
 08-MAR-1999
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| Human, PR01303 (UNG669) amino acid sequence SEG ID NO:1394.
| Maint, PR01303 (UNG669) amino acid sequence SEG ID NO:1394.
| Modernan, PR01303 (UNG669) amino acid sequence SEG ID NO:1394.
| Modernan, PR01304 (UNG669) amino acid sequence SEG ID NO:1394.
| Modernan, PR01305 (UNG669) amino acid sequence SEG ID NO:1394.
| Modernan, PR01306 (UNG669) amino acid sequence SEG ID NO:1394.
| Modernan, PR01306 (UNG669) amino acid sequence SEG ID NO:1394.
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| Modernan, PR01306 (UNG669) amino acid sequence SEG ID NO:1394.
| Modernan, PR01306 (UNG69149) amino acid sequence SEG ID NO:1394.
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| Modernan, PR01306 (UNG69149) amino acid sequence SEG ID NO:1394.
| Modernan, PR01306 (UNG679) amino acid sequence SEG ID NO:1394.
| Modernan, PR01306 (UNG679) amino acid sequence SEG ID NO:1394.
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| Modernan, PR01306 (UNG679) amino acid sequence SEG ID NO:1394.
| Modernan, PR01306 (UNG679) amino acid sequence SEG ID NO:1394.
| Modernan, PR01306 (UNG679) amino acid sequence SEG ID NO:1396.
| Modernan, Moder
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Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition.
 AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AAY99340 to AAX99462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding then have various industrial applications, including uses as pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCF primers and hybridisation probes used in the isolation of the PRO polypeptides from the present invention
 TSNMVCAGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDW
 MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTA
 MGLSIFLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTA
 SSVQPLPLPUDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI
 AHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRV
 TSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI
 Length 248;
 Indela
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 receptor/ligand
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 Query Match
Best Local Similarity 100.0%; Pred. No. 3.8e-98;
Matches 248; Conservative 0; Mismatches 0;
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 Werhman T;
 ID NO:
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 Qian XB,
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 English
 248
 encoded protein SEQ
 2000US-00491404.
2000US-00617746.
2000US-00631451.
2000US-00663870.
 2001WO-US002687
 standard; protein;
 Zhou P,
1, Zhang
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 Drmanac RA,
 Fig 108;
 INC
 IRMIMENN
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 Liu C,
 Sequence 248 AA;
 WO200154477-A2
 HYSEQ
 25-JAN-2000;
17-JUL-2000;
03-AUG-2000;
15-SEP-2000;
 25-JAN-2001;
 sapiens
 02-AUG-2001.
 12-OCT-2001
 Human EST
 Claim 12;
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98US-0103318P

98US-0103318P

98US-0103318P

98US-0103633P

98US-0103633P

98US-0105693P

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98US-0105691P

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98US-010885P
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 mammalian DNA polypeptides,
 WPI; 2000-237871/
N-PSDB; AAA37075.
30-SEP-1998;
01-OCT-1998;
02-OCT-1998;
02-OCT-1998;
06-OCT-1998;
07-OCT-1998;
07-OC
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 Sequence 248 AA;
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06-JAN-2000;
 17-SEP-2003
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fly, sea
 RLLRLRLPVRV
 PNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI
 TSNMVCAGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDW
 VLIDHRWVLTA
 RLLRLRLPVRV
 TSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI
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 The present invention provides the protein and coding sequence proteins from a variety of organisms, including human, dog, ca cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly urchin and tomato. These were derived from expressed sequence from the organism of interest. They can be used in diagnostics forensics, gene mapping, identification of mutations, to asses biodiversity and for nutritional purposes. The present sequence protein of the invention
 48
 diagnostics
 Ŕ
 1 MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGG
 AHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDL
 AHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDL
 Length
 Indels
 Score 1374; DB 4;
Pred. No. 3.8e-98;
Mismatches 0;
 diseases,
 Page 1048-1049; 1275pp; English.
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 therapy
 for treatment
 AAB66142 standard; protein; 248 AA
 0
 transmembrane; gene
 99US-0141037P.
99US-0144758P.
99US-0145698P.
99WO-US020111.
99WO-US028313.
99WO-US028551.
 100.0%;
 2000WO-US004342
 invention #54
 research use
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 processing, hambeed toward, The urchin and toward. The
 248
 Isolated polypeptide antibodies and resea
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 WPI; 2001-476164/51
N-PSDB; AAH98653.
 l Similarity
248; Conser
 SSVOPLPL
 IRMIMRNN
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 Sequence 248 AA;
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 WO200078961-A1
 23-JUN-1999;
20-JUL-1999;
26-JUL-1999;
01-SEP-1999;
29-OCT-1999;
30-NOV-1999;
02-DEC-1999;
 18-FEB-2000;
 Unidentified
 28-DEC-2000
 02-APR-2001
 of
 Secreted;
 Claim 20;
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The nucleic
 ic acids designated PRO, and gene mapping and gene
 Human; secreted and transmembrane protein; PRO; angiogenesis; endothelial cell proliferation; wound healing; immune response; T-lymphocytes proliferation; neonatal heart hypertrophy; tumour; cardiac insufficiency disorder; calcium flux; inflammation; wascular endothelial growth factor-stimulated proliferation; mammalian kidney mesangial cell proliferation; Berger disease; nephropathy; Schanlein-Henoch purpura; celiac disease; Crohn's disease, dermatitis herpetiformis; diabetes; haemoglobin switch; insulinaemia; pancreatic beta-cell precursor cell differentiation; thalassemias; obesity; auditory hair cell regeneration; hearing loss; bone disorder;
 Fong S;
Hillan KJ;
Watanabe
 The present invention relates to secreted and transmembrane proteins. These proteins and the DNA encoding them may be used as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. They may also be used used to generate either transgenic animals or knockout animals which are in turn useful for development and screening of therapeutically useful reagents. The nuclacids may also be used in gene therapy
 MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTA
 AHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRV
 TSNMVCAGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDW
 AHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRV
 TSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI
 TSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI
 Gaps
 ٥;
 248;
 Ferrara N,
Gurney AL,
A, Tumas D,
 Length
 Indels
 Novel human secreted and transmembrane protein PRO1303.
 Baker KP, Botstein D, Desnoyers L, Eaton DL, I
Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gi
Pan J, Paoni NF, Roy MA, Smith V, Stewart TA,
Williams PM, Wood WI;
 Score 1374; DB 4;
Pred. No. 3.8e-98;
Mismatches 0;
 and nucleic chromosome ar
 ed and transmembrane proteins as hybridization probes, in o
 ABO33635 standard; protein; 248 AA.
 Claim 1; Fig 108; 787pp; English
 0;
 Query Match
Best Local Similarity 100.0%;
Matches 248; Conservative (
2000WO-US000219
2000WO-US000376
 entry)
 (GETH) GENENTECH INC
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98US-0103258P.
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98US-0103314P.
98US-0103315P.
98US-0103315P.
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 06-OCT-1998;

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 arthritis
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 98US-0098716P.
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98US-0102571P.
98US-0102571P.
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 disorder; sports
 2001US-000158
 US2003073130-A1
 sapiens
 -DEC-2001
 -APR-2003
 cartilage
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antidiabetic; anorectic; antiarthritic; angiogenesis; cancer; adrenal cortical capillary; endothelial cell growth; wound healing; stimulated T-lymphocyte proliferation; immune response suppression; neonatal heart hypertrophy; cardiac insufficiency disorder; vascular endothelial growth factor; inflammation; mononuclear cell; eosinophil; diabetes; obesity; or hyper-insulinaemia; hypo-insulinaemia; chondrocyte redifferentiation; bone disorder; cartilage disorder; sports injury; arthritis.
 98US-0098716P.
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98US-0102240P.
98US-0102307P.
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 2001US-00006B56
 US2003044841-A1
 01-SEP-1998;

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 Fong S;
Hillan KJ;
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 CLNLSIVSH
 ad PRO polypeptides e.g. PRO1130, PRO1275, PRC modulate glucose or free fatty acid uptake by, and are useful for treating diabetes, hyper-
 Length
 Indels
 transmembrane protein; PRO;
 Score 1374; DB 6;
Pred. No. 3.8e-98;
Mismatches 0;
 GWGITNHPRNPFPDLL
 Botstein D, Desnoyers L, Eaton DL, dard A, Godowski PJ, Grimaldi JC, ni NF, Roy MA, Smith V, Stewart TA
 secreted/transmembrane protein PRO1303
 248 AA
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 Query Match
Best Local Similarity 100.0%;
Matches 248; Conservative 0;
2000WO-US000376.

2000WO-US003565.

2000WO-US005004.

2000WO-US005841.

2000WO-US005841.

2000WO-US013705.

2000WO-US013705.

2000WO-US013705.

2000WO-US013264.

2000WO-US015264.

2000WO-US015264.

2000WO-US023522.

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2000WO-US023522.

2000WO-US023678.

2001WO-US036666.

2001WO-US0317800.

2001WO-US017800.

2001WO-US017835.

2001WO-US01735.
 standard; protein;
 Human; secreted protein;
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WI;
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 Goddard A,
Paoni NF, I
 WPI; 2003-585293/55
N-PSDB; ACD68378.
 IRMIMENN
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 Novel isolated PRO1787 that moments muscle cells, a
 06-JAN-2000;

11-FEB-2000;

24-FEB-2000;

02-MAR-2000;

15-MAR-2000;

17-MAY-2000;

22-MAY-2000;

22-MAY-2000;

22-MAY-2000;

23-AUG-2000;

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 Williams PM,
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Fong S;
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Watanabe CK;
 MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTA
 TSNMVCAGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDW
 Gaps
 Novel secreted and transmembrane polypeptides and polynucleotides encoding them useful for treating various cardiac insufficiency disorders, bone and/or cartilage disorders such as sports injuries arthritis.
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 Ferrara N,
Gurney AL,
A, Tumas D,
 Length
 Indels
 L, Eaton DL, Grimaldi JC, Gv, Stewart TA,
 Score 1374; DB 7
Pred. No. 3.8e-98
0; Mismatches 0
 Baker KP, Botstein D, Desnoyers
Gao W, Goddard A, Godowski PJ,
Pan J, Paoni NF, Roy MA, Smith
Williams PM, Wood WI;
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99US-0145698P.
99WO-US0201111.
99WO-US021194.
99WO-US028313.
99WO-US028313.
99WO-US028551.
99WO-US028551.
2000WO-US000376.
2000WO-US000376.
2000WO-US0003565.
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2000WO-US013678.
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Gurney AL,
A, Tumas D
 Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, preparation of a medicament for treating a condition respondlypeptide, and as therapeutic agents e.g. vaccines.
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Grimaldi JC,
I V, Stewart TA
 Score 1374; DB Pred. No. 3.8e-9; Mismatches
 escribes an isolated E
, having at least 80%
 KP, Botstein D, Desnoyers
Goddard A, Godowski PJ,
Paoni NF, Roy MA, Smith
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99US-0129674P.
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99WO-US028513.
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Matches 248; Co
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25-SEP-1998;
27-OCT-1998;
27-OC
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The invention relates to human PRO polypeptides and the polynucleotides encoding them. The sequences are useful in the preparation of a medicament for treating a condition responsive to a PRO polypeptide. The polypeptides are useful in a number of functional biological assays, as molecular weight markers for protein electrophoresis and as therapeutic
 Fong S;
Hillan KJ;
Watanabe C
 61 AHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRV
 GLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTA
 e.g. PRO1491 and PRO1571, useful treating a condition responsive tagents e.g. vaccines.
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 Ferrara N,
Gurney AL,
A, Tumas D,
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 Indels
 L, Eaton DL, F
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 GENENTECH INC
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3; obesity;
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 -DEC-2001
 9-MAY-2003
 15-JAN-2004
 241
 ADD70709
 ADD70709
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 Human; secreted protein; transmembrane protein; PRO; tumour; immune response; cardiac insufficiency disorder; calcium flux; umbilical vein endothelial cell; bone disorder; cartilage disorder; arthritis; wound healing; diabetes; skeletal muscle cells; obesity; Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease; dermatitis; herpetiformis; Crohn's disease; thalassaemia.
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Score 1374; DB 7;
Pred. No. 3.8e-98;
Mismatches 0;
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 248
 99WO-US020111.

99WO-US0201111.

99WO-US028313.

99WO-US028313.

99WO-US028551.

2000WO-US000219.

2000WO-US000376.

2000WO-US003565.

2000WO-US004342.

2000WO-US004342.

2000WO-US004342.

2000WO-US004342.

2000WO-US014041.

2000WO-US014042.

2000WO-US014941.

2000WO-US014941.

2000WO-US014941.

2000WO-US014042.

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2000WO-US014042.

2000WO-US014941.

2000WO-US014042.

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21-NOV-2000;
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 01-MAY-2003.
 15-JAN-2004
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 PRO1418, PRO1555,
y skeletal muscle
hypo-insulinemia.
 Fong S;
Hillan KJ;
Watanabe CK;
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 (secreted
 Ferrara N
Gurney AL,
A, Tumas D
 l PRO polypeptides e.g., PRO1130, PRO1275, Pl
glucose or free fatty acid (FFA) uptake by
useful for treating diabetes or hyper- or hy
 polypeptide
 TA,
 L, Eaton DL,
Grimaldi JC,
V, Stewart TA
 PRO
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 n D, Deenoyers Godowski PJ, Roy MA, Smith WI;
 553pp;
 98US-0108775P.
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98US-0108775P.
98US-010878P.
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99US-01080989P.
99US-01800-US006666.
2000WO-US013705.
2000WO-US013705.
2000WO-US013705.
2000WO-US013705.
2000WO-US013705.
2000WO-US013705.
2000WO-US0130873.
2000WO-US0130873.
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 194;
 relates
 INC
 P, Botstein I
Goddard A, (
Paoni NF, Rd
S PM, Wood WI
 ID NO
 81
 GENENTECH
 WPI; 2003-874602/
N-PSDB; ADD70708.
 isolated
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 invention
 10-NOV-1998;
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Pan J,
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98US-0100849P.
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98US-0101068P.
98US-0101071P.
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 06-DEC-2001;
 15-JAN-2004
 20-MAR-2003
 241
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 181
 ADD70232
 Ношо
 RESULT
 ADD702
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A
 The invention relates to an isolated PRO polypeptide (secreted or transmembrane protein) having at least 80% amino acid sequence identity transmembrane protein) having at least 80% amino acid sequence as given in the specification (including their extracellular domains either or without their associated signal peptides. Also include are the nucleotide (NA) sequences encoding PRO, a vector comprising the PRO NA, a host cell comprising the vector, producing PRO, a chimaeric molecule comprising PRO fused to a heterologous amino acid sequence, and an antiper properties and also for chromosome identification. PRO is also useful for tissue typing. PRO and PRO NA are useful for tissue typing. PRO and PRO NA are useful for tissue typing. PRO and PRO NA are useful for tissue typing. PRO and RO NA are useful in development and screening useful reagents. PRO NA is also useful in development and screening useful reagents. PRO NA is also useful in development and screening useful reagents. PRO NA is also useful in gene therapy. PRO1244, PRO1256 and PRO1410 polypeptide are useful for repating cardiac insufficiency disorders. PRO1246 polypeptide are useful for treating cardiac insufficiency disorders. PRO126 polypeptide are useful for treating diabetes. PRO1374 polypeptides are useful for treating diabetes in skelteral mach control numbilical vent endertheilal cells. PRO1256, PRO1275 and PRO1418 polypeptides are useful for treating diabetes in skelteral mach cells and obesity. PRO1265, PRO1264 and PRO1382 polypeptides are useful for treating diabetes in skelteral mach properties are useful for treating diabetes in skelteral mach properties are useful for treating benefit some contern nephropathies ascentised with Schonlein-Hench purpurs, coellac disease, dermakeltis, herpetiformis or Crohn disease. PRO1478, PRO1265, PRO1418, PRO1265, PRO1418, PRO1265, PRO1418, PRO1265, PRO1418, PRO1265, PRO1418, PRO1265, PRO1418, PRO1265, PRO1418, PRO1265, PRO1418, PRO1265, PRO1418, PRO1265, PRO1418, PRO1265, PRO1418, PRO1265, PRO1418, PRO126
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 Fong S;
Hillan KJ;
Watanabe CK;
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 01
 DLRLLRLRLPVRV
 PGVYTYICKYVDW
 3GVLIDHRWVLTA
 GGVLIDHRWVLTA
 SHATCHGVYPGRI
 New secreted and transmembrane PRO polypeptides useful for treating cancers, kidney disorders, Crohn's disease, diabetes mellitus, hyper-hypo-insulinemia, sports injuries and arthritis.
 Gaps
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 248
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Gurney AL,
 MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRC
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 Length
 Indels
 TSNMVCAGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGI
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A, Smith V, Stewart TA,
 Score 1374; DB 7;
Pred. No. 3.8e-98;
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 .,
 .P, Botstein D, Desnoz
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 100.0%;
larity 100.0%;
Conservative 0
2001WO-US006666.
2001WO-US017800.
2001WO-US019692.
2001WO-US021066.
2001WO-US021735.
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20-JUN-2001;
29-JUN-2001;
 Williams PM,
 09-JUL-2001;
 248;
 181
 Claim 12;
 19
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 121
 121
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 Query Match
Best Local
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 (GETH)
 Gao W,
 Baker
 Matches
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Human; secreted protein; transmembrane protein; PRO; tumour; immune response; cardiac insufficiency disorder; calcium flux; umbilical vein endothelial cell; bone disorder; cartilage disorder; arthritis; wound healing; diabetes; skeletal muscle cells; obesity; Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease; dermatitis; herpetiformis; Crohn's disease; thalassaemia.
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Fong S;
Hillan KJ;
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 modulating
in protein
 or
 polypeptide (secreted
 .
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 248
 Ferrara N,
Gurney AL,
A, Tumas D,
 typing,
markers
 Length
 Indele
 TA,
 Novel isolated PRO polypeptide useful for tissue biological activity of cell, as molecular weight electrophoresis, for treating arthritis, tumor.

 n D, Degnoyerg L, Eaton DL,
Godowski PJ, Grimaldi JC,
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WI;
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99US-01080-US03267P.
90UWO-US03267P.
90UWO-US03267P.
90UWO-US03267P.
90UWO-US019692.
 194;
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 biological activity o
electrophoresis, for
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N-PSDB; ADD70231.
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 Paoni NF,
 SEO
 The invention
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23-JUN-1999;

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25-JUN-1999;

26-JUL-1999;

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26-JUN-2001;

29-JUN-2001;

29-JUN-2001;
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 Gao W,
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98US-0100711P.
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 rous tumors, mellitus,
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 Ferrara N,
Gurney AL,
A, Tumas D,
 for treating cance
healing, diabetes
 relates to an isolated PRO polypeptide protein) having at least 80% amino acid
 Grimaldi JC, Gu
V, Stewart TA,
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 Novel isolated PRO polypeptide, cardiac insufficiency disorders, thalassemias.
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Fong S; Hillan KJ; Watanabe CK; Ferrara N, Gurney AL, 1, Tumas D, TA, Baker KP, Botstein D, Desnoyers L, Eaton DL, Gao W, Goddard A, Godowski PJ, Grimaldi JC, Pan J, Paoni NF, Roy MA, Smith V, Stewart TF

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 Novel isolated PRO polypeptide useful for tissue biological activity of cell, as molecular weight electrophoresis, for treating arthritis, tumor.
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Matches 248; Conservative 0; Mismatches 0;
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